

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 11:05:10 ; Search time 93 Seconds

(without alignments)
881.793 Million cell updates/sec

Title: US-09-841-741-2

Sequence: 1 MTSTCTNSTRENSNSHTCMP.....GTGEGTEGKIYPSYDSATFP 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_oranella:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2024	96.7	508	4 Q96P66	Q96P66 homo sapien
2	430.5	20.6	402	13 Q90X46	Q90X46 brachydiano
3	430	20.5	407	4 Q75963	Q75963 homo sapien
4	376	18.0	425	6 Q9MZU2	Q9MZU2 oryctolagus
5	376	18.0	429	6 Q9MZU3	Q9MZU3 oryctolagus
6	376	18.0	466	4 Q96RE8	Q96RE8 homo sapien
7	371.5	17.7	445	4 Q60451	Q60451 homo sapien
8	366.5	17.5	429	4 Q13729	Q13729 homo sapien
9	366.5	17.5	499	4 Q13675	Q13675 homo sapien
10	358.5	17.1	466	4 Q9UD63	Q9UD63 homo sapien
11	357	17.1	466	4 Q9TSM7	Q9TSM7 sus scrofa
12	343.5	16.4	408	13 Q98998	Q98998 xenopus lae
13	330.5	15.8	349	4 Q9UD67	Q9UD67 homo sapien
14	325	15.5	391	5 Q96716	Q96716 brachyosco
15	321	15.3	571	6 Q9TWM9	Q9TWM9 sus scrofa
16	320.5	15.3	422	6 Q9N298	Q9N298 pan troglod

17	320.5	15.3	422	6 Q9N297	Q9N297 gorilla gor
18	319	15.2	515	11 Q9DBL0	Q9DBL0 mus musculus
19	315.5	15.1	422	6 Q9N296	Q9N296 ponga pygma
20	315	15.1	518	6 Q9MT18	Q9MT18 oryctolagus
21	312.5	14.9	559	11 Q9QW71	Q9QW71 ratu
22	306	14.6	447	6 Q8SPH2	Q8SPH2 sus scrofa
23	305.5	14.6	419	5 Q77254	Q77254 boophilus m
24	301.5	14.4	508	5 Q9NH3	Q9NH3 alysi
25	301	14.4	508	5 Q9VC23	Q9VC23 alysi
26	299.5	14.3	394	5 Q9N156	Q9N156 diosop
27	299	14.3	470	11 P97842	P97842 ratu
28	288	13.8	445	4 Q9N2R3	Q9N2R3 homo
29	286	13.7	370	4 Q9H1N4	Q9H1N4 homo
30	285	13.6	443	4 Q9UDP9	Q9UDP9 homo
31	280.5	13.4	392	13 Q9YHA5	Q9YHA5 myxine
32	276.5	13.2	354	13 P87496	P87496 xenopus
33	276	13.2	430	5 Q19449	Q19449 caen
34	273.5	13.1	534	13 Q57422	Q57422 xenopus
35	272.5	13.0	414	6 Q96K99	Q96K99 canis
36	271.5	12.9	367	13 Q9DG47	Q9DG47 esox
37	270.5	12.9	372	13 P79945	P79945 xenopus
38	270	12.9	387	4 Q96KH9	Q96KH9 homo
39	270	12.9	387	4 Q96K10	Q96K10 homo
40	269.5	12.9	388	13 Q9G054	Q9G054 brachy
41	269	12.9	464	5 Q9G054	Q9G054 aedes
42	269	12.9	474	4 Q96RG8	Q96RG8 homo
43	268.5	12.8	405	11 Q9CRR2	Q9CRR2 mus
44	268.5	12.8	414	6 Q9GKAO	Q9GKAO canis
45	267.5	12.8	413	4 Q96EC3	Q96EC3 homo

ALIGNMENTS

RESULT 1
Q96P66 PRELIMINARY; PRT; 508 AA.
ID Q96P66
AC Q96P66;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE G protein-coupled receptor (Putative G-protein coupled receptor).
GN GPR101 OR GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=2145857; Pubmed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes";
RL Gene 275:83-91(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF411115; AAL26486.1; -;
DR EMBL: AB083588; BAB89301.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 508 AA; 56716 MW; E20A409F65C95B5 CRC64;

Query Match 96.7%; Score 2024; DB 4; Length 508;
Best Local Similarity 78.1%; Pred. No. 7.6e-179;
Matches 397; Conservative 1; Mismatches 0; Indels 110; Gaps 1;

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QY 1 MESTCTNSPPSSSHTCMPLSPMISLAHGIIRSTVIVIFLAASFVGNIVLALVQRP 60
Dh 1 MISTCTNSPPSSSHTCMPLSPMISLAHGIIRSTVIVIFLAASFVGNIVLALVQRP 60
QY 61 QLLQVTRNFIPLNLVTDLQISIVAPWVATSVLPFWPLNSHFCALVSLTHLFAFASV 120
Dh 61 QLLQVTRNFIPLNLVTDLQISIVAPWVATSVLPFWPLNSHFCALVSLTHLFAFASV 120
QY 121 TTVVSVVRPYLSIHPPLSPSKMTQPPGYLLLYGTWIVALTOSTPPLYMGQAAPFPRNA 180
Dh 121 TTVVSVVRPYLSIHPPLSPSKMTQPPGYLLLYGTWIVALTOSTPPLYMGQAAPFPRNA 180
QY 181 LGSMTWGAASPYTILSVSVFVIFLVIACSVVFCARROHALLYNVGRHSLEVRKD 240
Dh 181 LGSMTWGAASPYTILSVSVFVIFLVIACSVVFCARROHALLYNVGRHSLEVRKD 240
QY 241 CVENEDGAEKKEEFQDE----- 259
Dh 241 CVENEDGAEKKEEFQDE----- 259
QY 260 ----- 259
Dh 260 ----- 259
QY 301 PGSEVRESSIVASQSGMKGKBSSTVKEENSMAKDKGTEVNOCSIDLGEDMPEGEDDI 360
Dh 301 PGSEVRESSIVASQSGMKGKBSSTVKEENSMAKDKGTEVNOCSIDLGEDMPEGEDDI 360
QY 361 NPSDDVEAVNIPESLPSPRRNSNSNPPLPCYQCAKAVIFIIIFSVYSLGPYCEFLAV 420
Dh 361 NPSDDVEAVNIPESLPSPRRNSNSNPPLPCYQCAKAVIFIIIFSVYSLGPYCEFLAV 420
QY 371 EDSDHDLPGTEGTEGKIVPSYDSATFP 398
Dh 371 EDSDHDLPGTEGTEGKIVPSYDSATFP 398
QY 481 EDSHDLPGTEGTEGKIVPSYDSATFP 508
Dh 481 EDSHDLPGTEGTEGKIVPSYDSATFP 508

RESULT 2
Q90X46 PRELIMINARY: PRT: 402 AA.
AC 090X46:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DR 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
SC: b22015.4 (novel) protein similar to human G-protein coupled receptor
PE2
OS Brachydanio rerio (Zebrafish) (Zebrafish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
PN 11
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RI Submitted (0CT-2001) to the EMBL/GenBank/DBJ databases
RI EMBL: AL590146; GAC94897.1;
RI InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1.1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_1; 1.
KW Receptor.
SQ SEQUENCE 402 AA; 44373 MW; 5FB8875874267F0C CRC64;

Query Match 20.6%; Score 430.5; DB 13; Length 402.
Best Local Similarity 27.9%; Pred. No. 1,3e-31;
Matches 101; Conservative 78; Mismatches 138; Indels 45; Gaps 7;
QY 7 NSTPSSNSHTMPISFPMISLAHGIIRSTVIVIFLAASFVGNIVLALVQRP 66
Dh 6 NSTAVANSTNGIDENGLM-----VLESVSIILIIILACIGMLVIVVTLYKKRPYLLTPS 58

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QY 67 NRIENLVTDLQISIVAPWVATSVLPFWPLNSHFC--TALVSLTHLFAFASVNTIV 124
Dh 59 NRIENLVTDLQISIVAPWVATSVLPFWPLNSHFC--TALVSLTHLFAFASVNTIV 116
QY 125 VSDVRLSIHPPLSPSKMTQPPGYLLLYGTWIVALTOSTPPLYMGQAAPFPRNALCSM 184
Dh 117 IADRYVAALPYMTIPYMKITGNRAVLAIIVYIMLSHVLGCLPPLFGWSSFEPRFKMTCTV 176
QY 185 IWGASPSYTIILSVSVFVIFLVIACSVVFCARROHALLYNVGRHSLEVRKD 244
Dh 177 SWKEISYTAFTWVCCPLPVAMLVCGVIFRYARIRARKVY-----CGSVVS 226
QY 245 EDEGAEKKEEFQDEMNIPESLPSPRRNSNSNP-----LPCYQCAKAVIFIIIF 296
Dh 227 GEESSSGTR-----GPKSHSTSSGSPKSYIYEGSGQCYAFITTLIVVIG 271
QY 297 SYVSLGPYCEFLAVLAVVDVETQVPQWVITIIWFLQCCIHPPYVGYMKITKEIQ 356
Dh 272 TFLTWGPYVVVISTEALIGNSVSPQ-VETLVSWLSETSAVCHPLIYOLMKRYKELL 330
QY 357 DM 358
Dh 331 GM 332

RESULT 3
075963 PRELIMINARY: PRT: 407 AA.
AC 075963:
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DR 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE G-protein coupled receptor RE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
PN 11
RP SEQUENCE FROM N.A.
RA Raming K.;
RI Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RI EMBL: AF091890; AAC61598.1;
RI InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1.1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 407 AA; 45363 MW; 00078B8B5BC1F21 CRC64;

Query Match 20.5%; Score 430; DB 4; Length 407;
Best Local Similarity 29.8%; Pred. No. 1.5e-31;
Matches 101; Conservative 67; Mismatches 135; Indels 36; Gaps 9;
QY 31 GTRSTVIVIFLAASFV--GNIVLALVQRPQLQVTRNFIPLNLVTDLQISIVAPW 88
Dh 25 GVITTOPIAIVITIFPCIGMLVIVVTLYKRSYLLTLSNKFVSLTNFLSVLDPV 84
QY 89 VATSVPLFWPLNSHFCALVSLTHLFAFASVNTIVVSDRLSIHPPLSPSKMTQPPG 148
Dh 85 VTSSIPFEMIGVWVCHPSALLYLISASMLTIQVIAIDRYVAALPYMTIPYMTGARA 144
QY 149 YLLYGTWIVALTOSTPPLYMGQAAPFPRNALCSMTWGAASPYTILSVSVFVIFLVI 208
Dh 145 VMAIVYIMLSHVLGCLPPLFGWSSFEPRFKMTCTVAFWQIWCALPFLVW 204
QY 209 IACSVVFCARROHALLYNVGRHSLEVRKDQVENEDEGAEKKEEFQDEKNIFESLPP 268
Dh 205 LVYIGTIFPVAP-----VKAPYVHCITVIVIE-EDACPTGPYNS-----STSSSG 250
QY 269 SRPNS-----NSNPPLPCYQCAKAVIFIIIFSVYSLGPYCEFLAVLAV--VDVET 319

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Db 251 SPPNAGGVVYSAN-----QCKALITLVLVGAPMTWGPVYVVIASEALMGKSSVF 303
QY 320 QVPQWVITITITLFLQCCIHPPYVGYMHTTKKEIQDM 338
Db 304 SLETTA---TWLSFASAVCHPLIVGMKTKVKELLM 338

RESULT 4
Q9MZU2 PRELIMINARY; PRT; 425 AA.
ID Q9MZU2
AC Q9MZU2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Alpha 1a-adrenoceptor isoform 3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BREED NEW ZEALAND WHITE;
RX MEDLINE=20243335; PubMed=10780960;
RA Suzuki F., Taniguchi T., Takauji R., Murata S., Muramatsu I.;
RT "Splice isoforms of alpha(1a)-adrenoceptor in rabbit.";
FL Br. J. Pharmacol. 129:1569-1576(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF157505; AAF80168.1; -.
DR HSSP: P02699; 1P88.
DR InterPro: IPR002376; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ SEQUENCE 425 AA; 47009 MW; 1202C83BF7644CBF CRC64.

Query Match 18.0%; Score 376; DB 6; Length 425;
Best Local Similarity 28.1%; Pred. No. 1.5e-26;
Matches 102; Conservative 70; Mismatches 155; Indels 36; Gaps 8;

QY 7 NSTPSSNSHTCMPSKMPISLAHGIISTVIVIFLASFGVNIYALVLRPKPOLQYT 66
Db 7 NASDSSNCTH-----PPAPVNISKAILLGVILGILRGVILNIIIVILSVACHRHLSVT 61
QY 127 VDRYLSITIHPLSYSPSKMQRGRGYLLYGTWVAIIQSTPPLYGWGOAFDENNALCSMTW 186
Db 122 IDRYIGVGYPLRPYPTIVGRGLPALLCVMAFSLVSVGPLGWMQAPDD-ETTCOI-- 178
QY 187 GASPSYTLISVSVFIVPLIWIACYSVFCAPRQ---HALLVNKHSLSEVRKDCV 242
Db 179 NEEPGYVLSALGSEFYVPLTITLAMYCRVYVAVAKPESPGI.KSGLTDKDSQVTLPIHP 238
QY 243 ENEDEG-----AEKKEEFQDEMNIPESLPSSRRNSNSNPPLRCYOCKAAVIFIIIFS 297
Db 239 KNAFAGSGSVASAKKTHPSVRL-----LKPSREK-----KAAVTGLGIWGC 280
QY 298 VYLSLGPYCFGLAVLAWVDVETQVQWVITITLFLQCCIHPPYVGYMHTTKKEIQD 357
Db 281 FVLCLWLPF-FLVMPIGSFPPDKPPEIVFKIVFWLGYLNSCINPIIYPCSSQEFKAFQN 339
QY 358 MLK 360
Db 340 VLR 342

RESULT 5
Q9MZU3

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ID Q9MZU3 PRELIMINARY; PRT; 429 AA.
AC Q9MZU3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Alpha 1a-adrenoceptor isoform 2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BREED NEW ZEALAND WHITE;
RX MEDLINE=20243335; PubMed=10780960;
RA Suzuki F., Taniguchi T., Takauji R., Murata S., Muramatsu I.;
RT "Splice isoforms of alpha(1a)-adrenoceptor in rabbit.";
FL Br. J. Pharmacol. 129:1569-1576(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF157505; AAF80168.1; -.
DR HSSP: P02699; 1P88.
DR InterPro: IPR002376; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ SEQUENCE 429 AA; 47463 MW; F907B487CFE6D83B CRC64.

Query Match 18.0%; Score 376; DB 6; Length 429;
Best Local Similarity 28.1%; Pred. No. 1.6e-26;
Matches 102; Conservative 70; Mismatches 155; Indels 36; Gaps 8;

QY 7 NSTPSSNSHTCMPSKMPISLAHGIISTVIVIFLASFGVNIYALVLRPKPOLQYT 66
Db 7 NASDSSNCTH-----PPAPVNISKAILLGVILGILRGVILNIIIVILSVACHRHLSVT 61
QY 127 VDRYLSITIHPLSYSPSKMQRGRGYLLYGTWVAIIQSTPPLYGWGOAFDENNALCSMTW 186
Db 122 IDRYIGVGYPLRPYPTIVGRGLPALLCVMAFSLVSVGPLGWMQAPDD-ETTCOI-- 178
QY 187 GASPSYTLISVSVFIVPLIWIACYSVFCAPRQ---HALLVNKHSLSEVRKDCV 242
Db 179 NEEPGYVLSALGSEFYVPLTITLAMYCRVYVAVAKPESPGI.KSGLTDKDSQVTLPIHP 238
QY 243 ENEDEG-----AEKKEEFQDEMNIPESLPSSRRNSNSNPPLRCYOCKAAVIFIIIFS 297
Db 239 KNAFAGSGSVASAKKTHPSVRL-----LKPSREK-----KAAVTGLGIWGC 280
QY 298 VYLSLGPYCFGLAVLAWVDVETQVQWVITITLFLQCCIHPPYVGYMHTTKKEIQD 357
Db 281 FVLCLWLPF-FLVMPIGSFPPDKPPEIVFKIVFWLGYLNSCINPIIYPCSSQEFKAFQN 339
QY 358 MLK 360
Db 340 VLR 342

RESULT 6
Q9P88
ID Q9P88 PRELIMINARY; PRT; 466 AA.
AC Q9P88;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Adrenergic receptor alpha-1a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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DR PRINTS; PR00237; GPCRHDOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 429 AA; 47514 MW; A7B05C5D0A69B CRC64;

Query Match 17.5%; Score 366.5; DB 4; Length 429;
 Best Local Similarity 26.7%; Pred. No. 1.2e-25;
 Matches 108; Conservative 76; Mismatches 182; Indels 39; Gaps 10;

QY STRSNSHTCMPLSKMPLSLAHGIIRSTVIVFLAASVGNVLAVALYQRKQLQVYN 67
 DB SGNASDSSNCTOP--PAVNVISKAILLGLVILGLVGNILVILSVACHRHLSVTH 62
 QY 68 RFIENLVTDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLPFASVNTIVVSV 127
 DB 63 YIVNLAVADLLLTSTVLPFSAIFEVLGWAFGRVPCNMAAVDLCTASIMGLCTISI 122
 QY 128 DRYLSIHPLSPSKMTORRGYLLVGTWIVAILOSTPPLVGMGQAAFDERNALCSMIWG 187
 DB 123 DRYGVSYPLRPVITVQRGLMALCVWALSLVLSIGPLFGWQPA-PEDETICQI--N 179
 QY 188 ASPSYTLISVSVFIVPLIYMIACYSVFCARQ---HALLVNKRHSLEVRKDCVE 243
 DB 180 EEPGVYLFSAIGSFYLPALILVMYCPYVYAKPSPGLKSGKTDKSDSEVTLRIHRK 239
 QY 244 NEDEEG---AEKKEEFODEMNIPESLPPSRNSNSNPPLPCYQCKAAKVFIIIFSY 298
 DB 240 NAPAGSGMASAKTKTHFSVRL-----LKFSREK-----KAAKTGLIIVGCF 281
 QY 299 VLSGPGYCFPLAVLAVWVDETQVPOWVITIIIMLFLOCCIHPRVYGMHTTKKEIQDM 358
 DB 282 VLCMLPF-FLVMPIGSFPPDPKPSFTVFKIVFWLGYLNSCINPIIYPCSSQSFKKAFQNV 340
 QY 359 LKKFCKEKKPKEDS-----HPDLPGTEGTEGKI-VPSYDSATF 397
 DB 341 LRIOCLRRKQSSKHALGYTLHPSSQAVEGQHKDMVRIPVGSRETf 385

RESULT 9

Q13675 PRELIMINARY; PRT; 499 AA.

ID Q13675;
 AC Q13675;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Alpha 1C adrenergic receptor isoform 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP TISSUE=PROSTATE;
 RA Tanaka T.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE;
 RX MEDLINE=9525557; PubMed=7737411;
 RA Hirasawa A., Shibata K., Horie J., Takei Y., Obika K., Tanaka T.,
 RA Muramoto N., Takagaki K., Yano J., Tsujimoto G.;
 RT "Cloning, functional expression and tissue distribution of human alpha
 RT 1C-adrenoceptor splice variants";
 RL FEBS Lett. 363:256-260(1995).
 RP SEQUENCE OF 202-344 FROM N.A.
 RX MEDLINE=95104335; PubMed=7805763;
 RA Diehl N.L., Shreeve S.M.;
 RT "Identification of the alpha 1C-adrenoceptor in rabbit arteries and
 RT the human saphenous vein using the polymerase chain reaction";
 RL Eur. J. Pharmacol. 268:393-398(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL; D32202; BA06901.1; -;
 DR EMBL; S76001; AAD14205.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHDOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 SQ SEQUENCE 499 AA; 55000 MW; BA6B02B6192639D CRC64;

Query Match 17.5%; Score 366.5; DB 4; Length 499;
 Best Local Similarity 26.7%; Pred. No. 1.4e-25;
 Matches 108; Conservative 76; Mismatches 182; Indels 39; Gaps 10;

QY 8 STEBSNSHTCMPLSKMPLSLAHGIIRSTVIVFLAASVGNVLAVALYQRKQLQVYN 67
 DB SGNASDSSNCTOP--PAVNVISKAILLGLVILGLVGNILVILSVACHRHLSVTH 62
 QY 68 RFIENLVTDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLPFASVNTIVVSV 127
 DB 63 YIVNLAVADLLLTSTVLPFSAIFEVLGWAFGRVPCNMAAVDLCTASIMGLCTISI 122
 QY 128 DRYLSIHPLSPSKMTORRGYLLVGTWIVAILOSTPPLVGMGQAAFDERNALCSMIWG 187
 DB 123 DRYGVSYPLRPVITVQRGLMALCVWALSLVLSIGPLFGWQPA-PEDETICQI--N 179
 QY 188 ASPSYTLISVSVFIVPLIYMIACYSVFCARQ---HALLVNKRHSLEVRKDCVE 243
 DB 180 EEPGVYLFSAIGSFYLPALILVMYCPYVYAKPSPGLKSGKTDKSDSEVTLRIHRK 239
 QY 244 NEDEEG---AEKKEEFODEMNIPESLPPSRNSNSNPPLPCYQCKAAKVFIIIFSY 298
 DB 240 NAPAGSGMASAKTKTHFSVRL-----LKFSREK-----KAAKTGLIIVGCF 281
 QY 299 VLSGPGYCFPLAVLAVWVDETQVPOWVITIIIMLFLOCCIHPRVYGMHTTKKEIQDM 358
 DB 282 VLCMLPF-FLVMPIGSFPPDPKPSFTVFKIVFWLGYLNSCINPIIYPCSSQSFKKAFQNV 340
 QY 359 LKKFCKEKKPKEDS-----HPDLPGTEGTEGKI-VPSYDSATF 397
 DB 341 LRIOCLRRKQSSKHALGYTLHPSSQAVEGQHKDMVRIPVGSRETf 385

RESULT 10

Q9UD63 PRELIMINARY; PRT; 466 AA.

ID Q9UD63;
 AC Q9UD63;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Alpha adrenergic receptor subtype alpha 1C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94296402; PubMed=8024574;
 RA Weinberg D.H., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
 RA Borkowski D., Strader C.D., Bayne M.;
 RT "Cloning, expression and characterization of human alpha adrenergic
 RT receptors alpha 1a, alpha 1b and alpha 1c";
 RL Biochem. Biophys. Res. Commun. 201:1296-1304(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHDOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 SQ SEQUENCE 466 AA; 51514 MW; E4FB501531CFD59C CRC64;

Query Match 17.1%; Score 358.5; DB 4; Length 466;
 Best Local Similarity 26.4%; Pred. No. 76-25;
 Matches 107; Conservative 76; Mismatches 183; Indels 29; Gaps 10.

6
 8 STEENSHCHLSEMPISLANHIIIPSTVLVFLAASPVGNVLALVLEKPOLQAVTN 67
 5 GRNADGSSSTTEPFAVHISVAILDVLDLLEPGVGNRLVILVAGCHHLEVTH 62
 64 EFIEHLVTHLQTSVAWVAVATVFLFMHLNHSCTALVSLTHFAVSNTIVVSV 117
 63 YIVVLAVALDLTSTVLFPSALFEVLQVWAGVGNVMAVAVLCTVLSIMQLIISI 122
 122 IYVLSIIHHSVSPSTPEPQYLLVGTWVAIIQSTPRYQWQQAPEENALCSYIMG 187
 123 DRYIVSVYLRVITVTVGQGMALQVALSLVIVSISGLFPMQQAPEDETIQIIN 173
 189 APTSTTISVSPVIFVTVTAVAVCPAARQ...HALLVVPHSLEVVPQVVE 243
 180 EEPGVLPFSLQSFYLFELIILWVPRVVAVAFPSPLKPSJLKTQPSSEQVLP:HPK 239
 244 ENDEEGAEKKEEFGEMNIFESLPDSRNSNPLPPCYQCYAAVIFIIIFSY 298
 248 NAPAAPSMAKATTHRSVPL...LKFSPEK...KAAKTLGIVVQCF 281
 259 VLSLSPYCLAVLAWVAVETVQVWVITIIIMLFLOLCIHPRVVGVMKTIKEIOM 358
 282 VQGWLEFFLWPRIGSFFPRSETEVKIVFWLGYLNSCINIIYQSSQEFKACNV 340
 359 LKFSCEKEPPEDS...HPLFTEGTEGKI VESYDSATP 397
 341 LEICLPKQSSHALGYTLHPSLAVESGHELMVPIVOSDEFP 385

RESULT 11
 Q9TSW7 PRELIMINARY: PRT: 466 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Alpha-1A adrenergic receptor
 GN ALPHA-1A.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN NCBI_TaxID=9615.
 RP SEQUENCE FROM N.A.
 RA Uhlen S., Wraith A.
 PL "Characterization of the pig alpha-1A adrenergic receptor."
 PL Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases
 CC 1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
 CC 2. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
 DR EMBL, AJ251727, CAB65570.1, JOINED.
 DR EMBL, AJ251728, CAB65570.1, JOINED.
 DR InterPro: IPR000276; GPCR_Phospho.
 DR Pfam: PF00001; 7tm_1; 1
 DR PRINTS: PR00237; GPCRPhospho.
 DR PROSITE: PS00237, G-PROTEIN_RECEP_F1_1, 1.
 DR PROSITE: PS00262, G-PROTEIN_RECEP_F1_2, 1.
 KM G-protein coupled receptor, Glycophorin, Receptor, Transmembrane
 SO Sequence 466 AA, 51674 MW, AECVFE48A05A719C C0664.

Query Match 17.1%; Score 357; DB 6; Length 466;
 Best Local Similarity 26.2%; Pred. No. 9,76-25;
 Matches 107; Conservative 74; Mismatches 174; Indels 54; Gaps 13;

6
 7 NTFESNSRHTWFSMPISAHGIIIPSTVLVFLAASVGNVLALVLEKPOLQAVTN 66
 7 NTFESNSRHTWFSMPISAHGIIIPSTVLVFLAASVGNVLALVLEKPOLQAVTN 66
 67 NTFESNSRHTWFSMPISAHGIIIPSTVLVFLAASVGNVLALVLEKPOLQAVTN 66
 67 NTFESNSRHTWFSMPISAHGIIIPSTVLVFLAASVGNVLALVLEKPOLQAVTN 66

DB 63 HYIVLAVALDLTSTVLFPSALFEVLQVWAGVGNVMAVAVLCTVLSIMQLIISI 122
 CY 127 VERTLSIIHHSVSPSTPEPQYLLVGTWVAIIQSTPRYQWQQAPEENALCSYIMG 186
 DB 122 IERYIVSVYLRVITVTVGQGMALQVALSLVIVSISGLFPMQQAPEDETIQIIN 173
 CY 187 GASPSYLLSVSPVIFVTVTAVAVCPAARQ...HALLVVPHSLEVVPQVVE 243
 DB 179 KEETGYVLFSLQSFYVITIIIMVPRVVAVAFPSPLKPSJLKTQPSSEQVLP:HPK 239
 CY 243 ENDEEGAEKKEEFGEMNIFESLPDSRNSNPLPPCYQCYAAVIFIIIFSY 298
 DB 239 KPAIVQSSQWTSACKKHFVPL...LKFSPEK...KAAKTLGIVVQCF 281
 CY 259 VLSLSPYCLAVLAWVAVETVQVWVITIIIMLFLOLCIHPRVVGVMKTIKEIOM 358
 DB 282 VQGWLEFFLWPRIGSFFPRSETEVKIVFWLGYLNSCINIIYQSSQEFKACNV 340
 CY 359 LKFSCEKEPPEDS...HPLFTEGTEGKI VESYDSATP 397
 DB 341 LEICLPKQSSHALGYTLHPSLAVESGHELMVPIVOSDEFP 385

RESULT 12
 Q98998 PRELIMINARY: PRT: 408 AA.

DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE 5-HT1A receptor.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 RN NCBI_TaxID=8355.
 RP SEQUENCE FROM N.A.
 RA Tissue: BRAIN.
 FX MEDLINE=97364954, PubMed=9221903;
 RA Mariacci S., Cini D., Nardi I.;
 RT "Cloning and developmental expression of 5-HT1A receptor gene in
 RT Xenopus laevis."
 FT Mol. Brain Res. 47:67-77(1997)
 CC 1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
 CC 2. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
 DR EMBL, Y07901; CA66209.1, ...
 DR HSRP, F39274, 1MMH.
 DR InterPro: IPR000276; GPCR_Phospho
 DR Pfam: PF00001; 7tm_1; 1
 DR PRINTS: PR00237; GPCRPhospho.
 DR PROSITE: PS00237, G-PROTEIN_RECEP_F1_1, 1
 DR PROSITE: PS00262, G-PROTEIN_RECEP_F1_2, 1.
 KM G-protein coupled receptor, Glycophorin, Receptor, Transmembrane
 SO Sequence 408 AA, 45787 MW, ZCBQ156F7D38185 C0664.

Query Match 16.4%; Score 343.5; DB 13; Length 408;
 Best Local Similarity 25.4%; Pred. No. 1,56-23;
 Matches 100; Conservative 67; Mismatches 160; Indels 59; Gaps 8;

DB 24 SCVPS--YQIIASLFLQSFSGAGFGNACVAVATNER--SLGNVAVLIGSIATVIMV 79
 CY 81 ISLVAPWVAVSVLFWPLNHSCTALVSLTHFAVSNTIVVSVDEYLSIHPLSVP 140
 DB 80 SVLVPMANQVNVNKTWLSVTCVTHSLVLCSTSIHLCAALDRYMAITPDIIV 139
 CY 141 SKMTQSPGYLLVGTWVAIIQSTPRYQWQQAPEENALCSYIMGASPSYTLISVGF 200
 DB 140 NKPTPPAAVILSTIWIWFSISIPPMIGMPTP--ENRSDPNACVISEPQVTVISTFGA 197

QY 201 IYPLIYIACYSVFCARQHALLYNKRHSLEVRKVCYENEDDEGAKEKKEFODEM 260
Db 198 FYIPLILMLVLYGKILFKAR--FRIRKTYKAEKKKADTCLSVSQSGKEKQGAQOEL 255
QY 261 N-----IPESLPSSRRN- 272
Db 256 EEVGAQAQRCVNGAIRHGEAGVLEIEVHHVYNSKHLCKPAPPPQQLPALKNDGA 315
QY 273 SNSNPPLRCYCCKAKYIFIIISVYSLGRCFLAVLAWVDVETQVPCWYITIIWL 332
Db 316 TEARKKVALAPPEKTKVTLGIIMGTFLCMLPFIYALVLPFCET-CHMPLHLLDIITWL 374
QY 333 FFLQCCIHPPYVYVGMHKTKEIOMLKKPFCKE 366
Db 375 GYSNLSLNPITIAVFNKDPQSAFKIIRKCFKQ 408
RESULT 13
Q9UD67 PRELIMINARY: PRT: 349 AA.
AC Q9UD67
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Alpha 1C-adrenoceptor, alpha 1C-AR (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominda; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94254631; PubMed=8196478;
RA Faure C., Plomou C., Vallancien G., Langer S.Z., Graham D.,
RT "Identification of alpha 1-adrenoceptor subtypes present in the human
RT prostate.",
RL Life Sci. 54:1595-1605(1994).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00337; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 349 AA; 39361 MW; BAB3C09824EAC734 CRC64;
Query Match 15.8%; Score 330.5; DB 4; Length 349;
Best Local Similarity 27.4%; Pred. No. 2e-22;
Matches 96; Conservative 63; Mismatches 155; Indels 37; Gaps 9;
QY 62 LLOVNRFFNLVTDLQISLAPMVVATSVPLFPLNSHCTALVSLTLFAFASVNT 121
Db 6 LHSVHYIYVNLAVADLLTSTVLPFSAIEVLAQVAFGRVNCNMAADVACTCTASING 65
QY 122 IVVSVDRYLSIIHPLSYPSKMTORRGYLLVGTWIVALLQSTPLPYCGOAFDERNAL 181
Db 66 LCIIISIDRIGSYLRYTYITVQIRGLMALLCVALSLIVISIGLPGRQRA-PEDFTI 124
QY 182 CSMIGASPSYITLVSFTVPLIYIMACYSVVFCAARQ--HALLYVNRHSLEVR 237
Db 125 CQI--NEEGYVLFSAIGFYPLAIIILVMYCRYVYVAKRESRGLKSGIKTDSQVYT 182
QY 238 VVDCVENEDEEG--AEKKEPFODEMNIPESLPPSRNSNPNPLPRCYOCCAKYVF 292
Db 183 LRIRKKNAPAGSSMASAKTKTHFSVPL-----LKPSPK-----KAKTLTG 224
QY 293 IIFSYVLSLGRYCFCLAVLAWVDVETQVPCWYITIIWLFLQCCIHPPYVYVGMHKTIK 352
Db 225 IVVGFVLCWLF-FLVMDIGSFFPDKFSEYFKIVFVLGYNLCTINDIIVPCSSQERK 283
QY 353 KEIQMLKKFFCKEKPCKEDS-----HDDLPGEGTEGKI-VPSTDSATF 397

Db 284 KAFQNVLPICLPFKQSSKHALGTYLHPPSQAVFQGHKDMWPIFGSSETF 334
RESULT 14
Q96716 PRELIMINARY: PRT: 391 AA.
AC Q96716
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Dopamine D1/beta receptor.
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OC NCBI_TaxID=7740;
RN [1]
RP SEQUENCE FROM N.A.
RA Cardinaud B., Gilbert JM., Sugamori K.S., Coudouel S., Guibert B.,
RA Vincent J.D., Niznik H.B., Vernier P.,
RT "The amphioxus D1/beta receptor and the emergence of the vertebrate
RT adrenergic system.",
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ005433; CAA06536.1; -.
DR HSSP: P29274; 1MMH.
DR InterPro: IPR002106; AATRNA_ligaseli.
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00337; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1_1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 391 AA; 42622 MW; 67A5AD944AFA3FBE CRC64;
Query Match 15.5%; Score 325; DB 5; Length 391;
Best Local Similarity 25.8%; Pred. No. 7.3e-22;
Matches 96; Conservative 67; Mismatches 159; Indels 50; Gaps 8;
QY 2 TSTCTNSSTRESSSHTCMPLSKMPLSLAHGIRSVLYIFLAASVGNVIALVQRRQ 61
Db 10 TETNTANLSTSEASVSGCFAPNPYSAQVAVLGITVILLITVIGNVILAVTCHRK 69
QY 62 LLOVNRFFNLVTDLQISLAPMVVATSVPLFPLNSHCTALVSLTLFAFASVNT 121
Db 70 KRTVINPFLVSLACADLSGITVLPFAATNDLGYWPRGG-YCDVWVSFDVNSTASIIIN 128
QY 122 IVVSVDRYLSIIHPLSYPSKMTORRGYLLVGTWIVALLQSTPLPY-GW-----GQAAP 175
Db 129 LVVIAFDRLATATFFYHTFRTAGILITWGISLVVSFLPIQAGWYRDNQSEAL 188
QY 176 DEPNALCSMIGASPSYITLVSFTVPLIYIMACYSVVFCAARQHALLYNVRHSIE 235
Db 189 AIYSPCLCTIFASTAYITVSSLSIFYPILMLVFGIIFPAADQAR---KINALE 243
QY 236 VVDCVENEDEGAKEKEPFODEMNIPESLPPSRNSNPNPLPRCYOCCAKYVFII 295
Db 244 GRL-----EQNNNGKISLAKK-----KAKTLGITM 272
QY 296 FSYVLSLGRYCFCLAVLAWVDVETQVPCWYITIIWLFLQCCIHPPYVYVGMHKTKEI 355
Db 273 GVFIICWLPFFVYVIVNPPCD--PCVQPAVFALTMLGWINSCFNPDIYAF-----NKEF 325
QY 356 ODLKKFFCKE 367
Db 326 KVPVYKMITCHK 337
RESULT 15
Q9TM9 PRELIMINARY: PRT: 571 AA.
AC Q9TM9
DT 01-MAY-2000 (Tremblrel. 13, Created)

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01 MAY-2000 (Tremblrel. 13, Last sequence update)
01 MAR-2002 (Tremblrel. 20, Last annotation update)
DE Alpha-ID adrenergic receptor.
CN ALPHA-ID.
CS Sus scrofa (pig).
CC Eukaryota, Metazoa, Chordata, Craniota, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Cetartiodactyla, Suidae, Sus.
CX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Uhlen S., Wraith A.;
RT "Characterization of the pig alpha-1D adrenergic receptor.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
OC -1- SUBMITTER MAP LOCATION: INTERNAL MEMBRANE PROTEIN (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
DR EMBL; AJ250492; CAB59347.1; -
DR EMBL; AJ250493; CAB59347.1; JOINED
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00217; GPCR_Rhodopsn
DR PROSITE; PS00217; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 571 AA; 6084 MW; 8ACFF8C6C0A07281 CRC64;

Query Match 15.3%; Score 321; DB 6; Length 571;
Best Local Similarity 28.1%; Pred. No. 21;
Matches 97; Conservative 56; Mismatches 160; Indels 32; Gaps 10;

CY 29 AHGIIKSTLVVFLASFYGNIVLALVLRKPKQLVNTNRIENLVLTDLQISLVAPWY 88
DB 93 AGGVGVFLAFLMAVAGNLVLIVACNRHLQTVNPFIVNLAVADLLSATVLPFS 152
CY 89 VATSVPLFWPLNSHPTALVSLTHLPAFASVNTIVVSVDRPLSIHPLSYPSKMTQPRG 148
DB 153 ATMEVLGFMAFPAPFQVMAAVNVLCCTASITSLCTISVDRVYGVPHSLKYPSIMTEPKA 212
CY 149 VILLTGTWIVALLQSTPLPYQWQQAFLDPNALQSMIMASPSYITLSVSVFIVIPIV 207
DB 213 AAILALMAVAIVSVGPLGWEKEPVPDPER--FCGITEEA--GYAVFSLSGFFLPMAY 268
CY 268 WIAVYVVFCAAP FWHALLVNYVPHS-----LEVYKQVENEDE-EGA---EKKEE 255
DB 269 IVMYRGVVVAVAPSTTRSLFACVYRPPKASEVLPDHPGASTGDDPGHAMRSTKCHT 328
CY 256 FQTEENIIPESLPSPKSNNSNPPLPCYQCKAKVIFIIIFSYVLSLGPYCFVLAVLVWV 315
DB 329 FSSSLP-LIKESPEK-----KAAKTLAIVGVFVLCMPPEFFVLPFGS-L 373
CY 316 IVETQVPCVNVITIIITWLFLLCCIHRYVVGVMKTIKYEIQMLK 360
DB 374 FPQLKPESEGVFVIFWLVGYFNSGVNPLIYQSSPEFFPAFLRLLR 418

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Search completed: February 11, 2003, 11:10:12
 Job time : 96 secs


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FT TRANSMEM 144 168 4 (POTENTIAL).
FT DOMAIN 169 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 205 5 (POTENTIAL).
FT DOMAIN 206 272 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 273 297 6 (POTENTIAL).
FT DOMAIN 298 304 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 305 329 7 (POTENTIAL).
FT DOMAIN 330 466 CYTOPLASMIC (POTENTIAL).
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 7 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 466 AA: 51365 MW: 9446D356B50FCD0E CRC64:

Query Match 18.0%; Score 376; DB 1; Length 466;
Best Local Similarity 28.1%; Pred. No. 5, 1e-17;
Matches 102; Conservative 70; Mismatches 155; Indels 36; Gaps 8;

QY 7 NSTRESNHTCMPLSKMPSLAHGIRSTVLVFLAASFGVGNIVLALVQRKPOLQVT 66
DB 7 NASDSSNCTH-----PPAVNISKAILLGVLGGLIFGLVGLNIVLILSVACHRHLSVT 61
QY 67 NRFTNLVTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFAASVNTIVVS 126
DB 62 HYVIVNLAVADLLTSTVLPFSAIFETLGYMAFGVFCNIMAAVDVLCCTASTISLCVIS 121
QY 127 VDRVLSIHPILSYSPKMTQRCGLLYGTWIVAIIQSTPPLVYMGQAAPDERNALCSMW 186
DB 122 IDRYIGSVYPLFPYITVTPRGPLALCWAFSLVSVGLFGWRPAPDP-ETICQI-- 178
QY 187 GASPSYTLISVSPFVPLIPLIMVACSVVFCARQ---HALLVNKRSLSEVRYKDCV 242
DB 179 NEEPYVVFSAISGFYVPLTIIILAMYCRYVAVAKRESGKSLKTDKDSQEVTLRIHR 248
QY 243 ENEDEEG-----AEKKEEPQDEMNIPESLPSPRNSNSNPPLPRCQCRAKAYIFIIFS 297
DB 239 KNAPGSGSGVASAKKHTFSVRL-----LKFSREK-----KAAKTLGIVGVC 280
QY 298 YVLSIGPYCFVLAVVWVDETQVDPWVTIIIMFLFLOCCIHPPYVGYVHKTKKEIQD 357
DB 281 FVLGWLPLF-FLVMPIGSPFPDPKRPETVFKIVFWLGYLNSCINPIIYPCSSQCFKAFQN 339
QY 358 MLK 360
DB 340 VLK 342

RESULT 2
ALIA_HUMAN STANDARD; PRT; 466 AA.
AC P35348;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE adrenergic receptor).
AD AdRA1A or AMPALC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NRI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate; PubMed=8396931;
PX Hirasawa A., Horie K., Tanaka T., Takagaki K., Muzi M., Yano J.,
RA Teujimoto G.;
RT "Cloning, functional expression and tissue distribution of human cDNA
RT for the alpha 1C-adrenergic receptor.";
RL Biochem. Biophys. Res. Commun. 195:902-909(1993).
RP SEQUENCE FROM N.A.
RA Tseng-Crank J.C., Goetz A., Saussy D., Robertson K.M., Hazum S.,

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RA Haizlip J., Godinot N., Wisely B., Robertson C.N., Kost T.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes, and Hippocampus;
RX MEDLINE=94239386; PubMed=8183249;
RA Parry C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang R.,
RA Lepor H., Hartig P.R., Weinschenk R.L., Branchek T.A.,
RA Gluchowski C.;
RT "The alpha 1-adrenergic receptor that mediates smooth muscle
RT contraction in human prostate has the pharmacological properties of
RT the cloned human alpha 1C subtype."
RL Mol. Pharmacol. 45:703-708 (1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95114877; PubMed=7815325;
RA Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
RA Worman N.P., Campbell S., Fidock M.D., Furness L.M.,
RA Parry-Smith D.J., Peter B., Bailey D.S.;
RT "Cloning and pharmacological characterization of human alpha-1
RT adrenergic receptors: sequence corrections and direct comparison with
RT other species homologues";
RL J. Pharmacol. Exp. Ther. 272:134-142 (1995).
CC - FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC AND G(11) PROTEINS.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: HEART, BRAIN, LIVER AND PROSTATE, BUT NOT IN
CC KIDNEY, LUNG, ADRENAL, AORTA AND PITUITARY.
CC - PTM: CARBOXYL-TERMINAL SER OF THE RESIDUES MAY BE PHOSPHORYLATED
CC (BY SIMILARITY).
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, D25235; BAA04960.1; -
CC EMBL, U02569; AAA93114.1; -
CC EMBL, U03866; AAB60353.1; -
CC EMBL, L31774; AAB59486.1; -
CC Genew, HGNC:277; ADRA1A.
CC MIM, 104221; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50263; G-PROTEIN_RECEP_F2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 51 1 (POTENTIAL).
FT DOMAIN 52 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 88 2 (POTENTIAL).
FT DOMAIN 89 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 122 3 (POTENTIAL).
FT DOMAIN 123 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 167 4 (POTENTIAL).
FT DOMAIN 168 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 205 5 (POTENTIAL).
FT DOMAIN 206 272 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 297 6 (POTENTIAL).
FT DOMAIN 298 304 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 306 329 7 (POTENTIAL).
FT DOMAIN 330 466 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 22 23 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT MOD_RES 215 215 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 FT DISULFID 99 176 BY SIMILARITY.
 FT LIPID 345 345 PALMITATE (POTENTIAL).
 FT CONFLICT 43 43 G-> C (IN REF. 2).
 FT CONFLICT 129 129 C-> T (IN REF. 2).
 FT CONFLICT 347 347 C-> R (IN REF. 1 AND 4).
 FT CONFLICT 359 359 T-> P (IN REF. 2).
 FT CONFLICT 431 431 Q-> E (IN REF. 1).
 FT CONFLICT 442 442 S-> C (IN REF. 2).
 SQ SEQUENCE 466 AA; 51466 MW; 1A50487531DECDFF0 CRC64;

Query Match 17.7%; Score 371.5; DB 1; Length 466;
 Best Local Similarity 26.9%; Pred. No. 9.8e-17;
 Matches 109; Conservative 77; Mismatches 180; Indels 39; Gaps 11;

QY 8 STEENSSHTCMPLSKMPSISLAHGIIRSTVLVIFLAASFVGNIVLALVQKRPQLQVFN 67
 DB 5 SGNA SDSNCTQP--PAFVNISKALLGVILGGLIFGVLSNIVLVSACHRHLSVTH 62
 QY 68 RFTFNLLVTDLLQISLVAVWVAVTSVPLFWPLNSHCTALVSLTHLFAFASVNTIIVSV 127
 DB 63 YYIVNLAVADLLITSTVLPFSAIFEVLGYMAFGVFCNIMAAVDVLCCTASIMGLCTISI 122
 QY 128 DRYLSILHPLSYPSKMTORRGVYLLGYTWIVAILLOSTPPLYWGQAPDERNALCSMTWG 187
 DB 123 DRYIGVYPLRPYPTVITQRRGLMALLCWALSLVISIGPLFGMRQPA-PEDETTICQI--N 179
 QY 188 ASBSYTLISVSVFIVIPILVIMACYVVFCAARQ---HALLVNVKSHLEVRKDCV 243
 DB 180 EERGVYLFMSLGSFYLLPLAILVMYCRYVAVAKRSGKSLKTDKSDSEVYTLRIHRK 239
 QY 244 NEDEEG-----AEKKEFQDMNIPESLPBSRRNSNPPLPRCYQCAKAVYFTIISY 298
 DB 240 NADAGSGMASAKRTHTFVNL-----LKFSREK-----AAKTLGIIVGCF 281
 QY 299 VLSLGYCFPLAVLAWVDVETQVPOWVTITIIIMLFLOCCIHPRVYVGMHKIKKEIDM 358
 DB 282 VLCWLPF-FLVMPIGSFPPDPKSEIVFKIYFWLGYLNSCINPIITPSSQDFKAFQNV 340
 QY 359 LK-KFCKEKPKPK-----DSHPDLPGTGGTEGKI-VPSYDANP 397
 DB 341 LRIOCLCRKQSKRHALGYTLHPFSQAVEGQHKDMVRIPVSGRETF 385

RESULT 3
 A1AA_RAT STANDARD; PRT; 466 AA.
 ID A1AA_RAT
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C adrenergic receptor).
 DE ADRA1A OR ADRA1C.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Heart muscle;
 RX MEDLINE=95008062; PubMed=7923624;
 RA Stewart A.F., Rokosh D.G., Bailey B.A., Karns L.R., Chang K.C., Long C.S., Kariya K., Simpson P.C.;
 RT "Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. Alpha 1C, alpha 1B, and alpha 1D mRNAs are present in cardiac myocytes but not in cardiac fibroblasts.";
 RL Circ. Res. 75:796-802(1994).
 RN [2]

SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=95021119; PubMed=7953320;
 RA Laz T.M., Forray C., Smith K.E., Bard J.A., Vayssie P.J.,

RA Branchek T.A., Weinschenk R.L.;
 RT "The rat homologue of the bovine alpha 1C-adrenergic receptor shows the pharmacological properties of the classical alpha 1A subtype.";
 RL Mol. Pharmacol. 46:414-422(1994).
 CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q) AND G(11) PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL: U13368; AAA52103.1; -
 DR EMBL: U07126; AAA62866.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 27
 FT TRANSMEM 28 51
 FT DOMAIN 52 64
 FT TRANSMEM 65 88
 FT DOMAIN 89 99
 FT TRANSMEM 100 122
 FT DOMAIN 123 143
 FT TRANSMEM 144 167
 FT DOMAIN 168 181
 FT TRANSMEM 182 205
 FT DOMAIN 206 273
 FT TRANSMEM 274 297
 FT DOMAIN 298 305
 FT TRANSMEM 306 329
 FT DOMAIN 330 466
 FT CARBOHYD 7 7
 FT CARBOHYD 13 13
 FT CARBOHYD 22 22
 FT DISULFID 99 176
 FT MOD_RES 215 215
 FT LIPID 345 345
 FT CONFLICT 39 39
 FT CONFLICT 67 67
 SQ SEQUENCE 466 AA; 51597 MW; 4962D3A72E971A36 CRC64;

Query Match 17.7%; Score 371; DB 1; Length 466;
 Best Local Similarity 26.1%; Pred. No. 1.1e-16;
 Matches 106; Conservative 78; Mismatches 180; Indels 42; Gaps 10;

QY 7 NSTRENSHTCMPLSKMPSISLAHGIIRSTVLVIFLAASFVGNIVLALVQKRPQLQVFN 66
 DB 7 NASEBSNCTH-----PPAFVNISKALLGVILGGLIFGVLSNIVLVSACHRHLSVTH 61
 QY 67 NEFIFNLVTDLLQISLVAVWVAVTSVPLFWPLNSHCTALVSLTHLFAFASVNTIIVSV 126
 DB 62 HYIVNLAVADLLITSTVLPFSAIFEVLGYMAFGVFCNIMAAVDVLCCTASIMGLCTISI 121
 QY 127 VDRYSILHPLSYPSKMTORRGVYLLGYTWIVAILLOSTPPLYWGQAPDERNALCSMTWG 186
 DB 122 IDRYIGVYPLRPYPTVITQRRGLMALLCWALSLVISIGPLFGMRQPA-PEDETTICQI-- 178
 QY 187 GASBSYTLISVSVFIVIPILVIMACYVVFCAARQ---HALLVNVKSHLEVRKDCV 242

Db 179 NEEPGYVLSALGSFYVPLAIIIVMVCYVAVAKRESGLKSLKTDKSDSECVTLRIHR 238
 Cy 243 ENEDERG AEKKEEFQDSENNIPESLPSPRNSNSNPPLPCYCCAAKVFPIIIFES 297
 Db 239 KNPVAEQGGVSAKAKTHFSVRL-----LKFSREK-----YAAKTLGIWVGC 280
 Cy 298 YVLSLGYCFCLAVLAWVDVETQVPCWVITIIIMLFLOCCIHPRVYGYMKTIKKEIQD 357
 Db 281 FVLQMLPFP-FLVMPIGSPFPDPRKPSFETVKIVFWLGLYNSCINPIIYPCSSQSEFKAFON 339
 Cy 358 MLKKFFCKEKPPEKDS-----HPDLFGTEGTEGCKI-VPYSDSATP 397
 Db 340 VLPICLPFPQSSKHAIGYTLHPPSQAVEEGHGMWRIPVSGSETF 385

RESULT 4
 ALIAA MOUSE STANDARD; PRT; 466 AA.
 ID ALIAA MOUSE
 AC P97718; O54923; 36, Created
 DT 15-JUL-1998 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C adrenergic receptor).
 GN ADRA1A OR ADRA1C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Mus.
 NX NRII_Taxid=10090;
 RN [1]
 RC STRAIN=CD-1; TISSUE=Brain, and Kidney;
 RC MEDLINE=08292316; PubMed=3630362;
 RA Xiao L., Scofield M.A., Jeffries W.B.;
 RT "Molecular cloning, expression and characterization of cDNA encoding a mouse alpha1a-adrenoceptor";
 PL RT. J Pharmacol 194; 913-921 (1998)
 PN (2)
 PP SEQUENCE OF 197-280 FROM N A
 RC TISSUE=Brain;
 RX MEDLINE=96064818; PubMed=7595531;
 RA Alonso-Llamazares A., Zamantillo D., Casanova E., Gvalle S., Galvo P., Chinchetru M.A.;
 RT "Molecular cloning of alpha 1d-adrenergic receptor and tissue distribution of three alpha 1-adrenergic receptor subtypes in mouse";
 PL J Neurochem 65; 2387-2392 (1995).
 CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIN SECOND MESSENGER SYSTEM ITS EFFECT IS MEDIATED BY G(Q)
 CC AND G(11) PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: CARBOXYL-TERMINAL SER OR THR RESIDUES MAY BE PHOSPHORYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: RELINGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS

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 CC -----
 DR EMBL: AF031431; AAC02658.1; -
 DR EMBL: S80220; AAB47044.1; ALT_INIT.
 DR MGD: MGI:104773; Adrala.
 DR InterPro: IPR000276; GPCR_Phosphn
 DR Pfam: PF00001; 7tm_1, 1
 DR PRINTS: PR00237; GPCRRCQDPSN.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 27
 FT TRANSMEM 28 51
 FT DOMAIN 52 64
 FT TRANSMEM 65 88
 FT DOMAIN 89 99
 FT TRANSMEM 100 122
 FT DOMAIN 123 143
 FT TRANSMEM 144 167
 FT DOMAIN 168 181
 FT TRANSMEM 182 205
 FT DOMAIN 206 273
 FT TRANSMEM 274 297
 FT DOMAIN 298 305
 FT TRANSMEM 306 329
 FT DOMAIN 330 466
 FT CARBOHYD 7 7
 FT CARBOHYD 13 13
 FT CARBOHYD 22 22
 FT MOD_RES 215 215
 FT DISULFID 99 176
 FT LIPID 345 345
 SQ SEQUENCE 466 AA; 51762 MW; 3649A5A3BD34DA CRC64;

Query Match 17.6%; Score 368; DB 1; Length 466;
 Best Local Similarity 27.1%; Pred. No. 1.6e-16;
 Matches 110; Conservative 75; Mismatches 179; Indels 42; Gaps 11;

Db 7 NSTPSSNSHTCMPLSLMPISLALGIIIPSTVIVFLAASFQNVILALVLPKQLQVT 66
 Db 7 NASGSGNTH---PPAONVSKA---ILGVTIIIGVLIIFGVANTLIVLSVACHPHLSVT 61
 Cy 67 NRPFFNLVTDLQISVAVFVAVATSVFLFPLNSHFECTALVSLTLFAPASVNTIVVVS 126
 Db 62 HYIVNLAVADLLTSTVLPESAIFELIGVAPSPVFENMAVADVLCSTMSIMGLCIS 121
 Cy 127 VDRYLSIHPSTYPSKMTOPPGVLLVGTWIVAILQSTPPVYGCQAAPDEPNALCSMTW 186
 Db 122 IDPYIGVSPVLPPTVITOPPGVALLCVMALSLVTSIGPLFGWQQA-PEDETTCQI- 178
 Cy 187 GASSTYTLVSSTVIVFLIMACYSVFCARPQ---HALLYNPHSEVAVPCV 242
 Db 179 NEEPGYVLSALGSFYVPLAIIIVMVCYVAVAKRESGLKSLKTDKSDSECVTLRIHR 238
 Cy 243 ENEDERG-----AEKKEEFQDSENNIPESLPSPRNSNSNPPLPCYCCAAKVFPIIIFES 297
 Db 239 KNPVAEQGGVSAKAKTHFSVRL-----LKFSREK-----YAAKTLGIWVGC 280
 Cy 298 YVLSLGYCFCLAVLAWVDVETQVPCWVITIIIMLFLOCCIHPRVYGYMKTIKKEIQD 357
 Db 281 FVLQMLPFP-FLVMPIGSPFPDPRKPSFETVKIVFWLGLYNSCINPIIYPCSSQSEFKAFON 339
 Cy 358 MLKKFFCKEKPPEKDS-----HPDLFGTEGTEGCKI-VPYSDSATP 397
 Db 340 VLPICLPFPQSSKHAIGYTLHPPSQAVEEGHGMWRIPVSGSETF 385

RESULT 5
 ALIAA CAURO STANDARD; PRT; 466 AA.
 ID ALIAA CAURO
 AC Q9WU25;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last sequence update)
 DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C adrenergic receptor).
 GN ADRA1A.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
 NX NBII_Taxid=10141;
 RN [1]
 RC SEQUENCE FROM N.A.

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RC TISSUE=Liver;
FX MEDLINE=21419075; PubMed=11527539;
RA Gonzalez-Espinosa C., Romero-Avila M.T., Mora-Rodriguez D.M.,
RA Gonzalez-Espinosa D., Garcia-Sainz J.A.;
RT "Molecular cloning and functional expression of the guinea pig
RL alpha1(a)-adrenoceptor";
RL Eur. J. Pharmacol. 426:147-156(2001).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC AND G(11) PROTEINS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF108016, AAC2540.2,
DR InterPro, IPR000276, GPCR_Rhodopsn.
DR Pfam, PF00001, 7tm_1, 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL 2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 25
FT TRANSSEM 26 51
FT DOMAIN 52 63
FT TRANSSEM 64 89
FT DOMAIN 90 99
FT TRANSSEM 100 122
FT DOMAIN 123 143
FT TRANSSEM 144 168
FT DOMAIN 169 181
FT TRANSSEM 182 205
FT DOMAIN 206 272
FT TRANSSEM 273 297
FT DOMAIN 298 304
FT TRANSSEM 305 329
FT DOMAIN 330 466
FT LIPID 345 345
FT CARBOHYD 7 7
FT CARBOHYD 13 13
FT SEQUENCE 466 AA; 51577 MW; E0E27E4FFED3D0CD CRC64;
SQ
Query Match 17.5%; Score 366.5; DB 1; Length 466;
Best Local Similarity 26.1%; Pred. No. 2e-16;
Matches 106; Conservative 75; Mismatches 184; Indels 41; Gaps 10;

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CY 298 YVLSLGFYCLAVLAWWDVENOVPCQWVITIIWLFLFOCTIPYVYGMYMKTKEIOD 357
DB 281 FVLQMLP-FLVMPIGSFFPDPRSEIVFKIVFWLGLVNSCLNPITIPGSSOEFKAFON 339
CY 358 MKKFECKEPEKPEKDS----HPDLPGTEGTEGKI-VPSYDAPF 397
DB 340 VLKIGCLPRKSSKHALGYTLHPPOAGVSGCKMDWRIPVSRFT 385

RESULT 6
A1AA BOVIN
ID A1AA BOVIN STANDARD; PRT; 466 AA.
AC P18130;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-1A adrenergic receptor (Alpha 1A-adrenoceptor) (Alpha-1C
DE adrenergic receptor).
GN ADRA1A OR ADRA1C.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90243698; PubMed=1970822;
RX Schwinn D.A., Lomasney J.W., Lorenz W., Szklut P.J., Fremieu R.T. Jr.,
RX Yang-Feng T.L., Caron M.G., Lefkowitz P.J., Cotecchia S.;
RT "Molecular cloning and expression of the cDNA for a novel alpha 1-
RT adrenergic receptor subtype";
RL J. Biol. Chem. 265:8183-8189(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92087349; PubMed=1966743;
RX Schwinn D.A., Cotecchia S., Lorenz W., Caron M.G., Lefkowitz R.J.;
RT "The alpha 1C-adrenergic receptor: a new member in the alpha 1-
RT adrenergic receptor family";
RL Trans. Assoc. Am. Physicians 103:112-118(1990).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM. ITS EFFECT IS MEDIATED BY G(Q)
CC AND G(11) PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, J05426, AAA0374.1, -
DR PIR, A35375, A35375.
DR InterPro, IPR000276; GPCR_Rhodopsn.
DR Pfam, PF00001, 7tm_1, 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL 2; 1.
KM G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 27
FT TRANSSEM 28 51
FT DOMAIN 52 64
FT TRANSSEM 65 88
FT DOMAIN 89 99
FT TRANSSEM 100 122
FT DOMAIN 123 143
FT TRANSSEM 144 167

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FT PMAIN 168 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 205 5 (POTENTIAL)
FT DOMAIN 206 273 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 297 6 (POTENTIAL).
FT PMAIN 298 305 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 306 329 7 (POTENTIAL).
FT PMAIN 330 445 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 7 7 N-LINKED (GLYCANC...) (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLYCANC...) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLYCANC...) (POTENTIAL).
FT MOD RES 215 215 PHOSPHORYLATION (BY PEA) (POTENTIAL).
FT DISULFID 99 176 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
SQ SEQUENCE 466 AA; 51466 MW; 77635153B39E5EC CRC64;

Query Match 17.0%; Score 356.5; DB 1; Length 466;
Best Local Similarity 25.5%; Pred. No. 8-16;
Matches 109, Conservative 74, Mismatches 176, Indels 65, Gaps 10;

CY 7 HCTFSSSHHTMPLSPKPSLSLHGIFSTVVFPAASFVSHVIALVIGPFTQLQVT 66
DB 7 KASSSSSNCH... PFFVNVSKALLSVITDGLIFVSGHIVILSVACHFHLSVT 61
CY 67 NEFFRLVTLQLSLVAFKVAIVSVLPFELNSHETALVSLTHLFAFASVNTIVVS 126
DB 62 HYYIVHLAVADLLTSTVLFPCAPELLCYMAFGVFCHVMAAVDVLCCTASIMGLIIS 121
CY 127 VHPVLSIHHSLSYSEKMTKPFVYLLVYTWIVALLSTPFLVWGGAEDFPAALGSMW 186
DB 122 IDRYGVSTFPLPPTVITVTKPDKMLVWALSLVLSISGLPFWPAPA-PEDETTDOI-- 178
CY 187 CASPSYTLISVSPFIVPLIWMACYSVVEFCARRO...HALLYVKKHSELEVRKDCV 242
DB 179 MEETVPLFSALGSEFVPLITLVMYGVVAVKPFGLPGLSKTCTFDSQVTLFHF 239
CY 243 ENEDEEG...AEKKEEGCEMNIPESLPSPRNSRNPRLPCGCCAAKVFITITSS 297
DB 239 PLAVVSRVSTSAKPTHTSVLE...LKFSREK...AAKTLGLVWAG 280
CY 208 VYLSGPGVFLVAVLWVVEVCPQWVITIIIMFLPLOCCHPYVYGVMHTIKKEIOD 357
DB 281 FVLCHLPLF-FLVMPKISFFPDRFSETVKIAWGLYLSNCINPIIYSSSGEFKARON 339
CY 358 MKKPKCFKPPY...EDSHDLP...PTEGEGEGKI 388
DB 340 VLPICLTPPKYSGKPTIGYTLHAPSHVFGCHDLVPIVGSASETPYKISYDGVCEWMI 399
CY 389 VPS 391
DB 400 PSS 402

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CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS ACTION BY
CC ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D63859; BAA09921.1;
CC InterPro: IPR000276; GPCR_Phodpsn.
CC Pfam: PF00001; Tem_1; 1.
CC FRITS, PR00237; GPCR_HODOPSIN.
CC DR PROSITE, PS00237; G-PROTEIN RECF_F1_1; 1.
CC DR PROSITE, PS00262; G-PROTEIN RECF_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family; Phosphorylation; Lipoprotein; Palmitate.
CY DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 28 51 1 (POTENTIAL).
FT DOMAIN 52 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 88 2 (POTENTIAL).
FT DOMAIN 89 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 122 3 (POTENTIAL).
FT DOMAIN 123 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 167 4 (POTENTIAL).
FT DOMAIN 168 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 205 5 (POTENTIAL).
FT DOMAIN 206 271 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 272 295 6 (POTENTIAL).
FT DOMAIN 296 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 327 7 (POTENTIAL).
FT DOMAIN 328 470 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 9 9 N-LINKED (GLYCANC...) (POTENTIAL).
FT CARBOHYD 12 12 N-LINKED (GLYCANC...) (POTENTIAL).
FT DISULFID 99 176 BY SIMILARITY.
FT LIPID 343 343 PALMITATE (POTENTIAL).
FT DOMAIN 351 354 POLY-HIS.
SQ SEQUENCE 470 AA; 51925 MW; D4F7A8303061D4E CRC64;

Query Match 16.9%; Score 354; DB 1; Length 470;
Best Local Similarity 26.0%; Pred. No. 1-2e-15;
Matches 109, Conservative 63, Mismatches 193, Indels 24, Gaps 10;

CY 12 SNSHTCPPLSTMPISLHAGTIRSTVLYFLAASFVGNIVLAVLQPKQLQVNTREIF 71
DB 11 SNCSHVLAP---ELNTYKAVAVLQWGLGIFLVYIGNILVLISVGRHLCQTVIYFIV 66
CY 72 NLVYDLDQLSLVAPWVAIVSVLPFELNSHETALVSLTHLFAFASVNTIVVSVDRL 131
DB 67 HLAVALDLSSVTLFFSALFELLCKRVEGFPVCHMAAAGVCCGASIMSGVSDRYI 126
CY 132 SLIHPLSPSKPTQSPGVLLLVGTWIVALLSTPFLVWGGAEDFPAALGSMWASPS 191
DB 127 GVSGLPYPAITKTPALLAVMLLWLSVVISIGPIFGWKPBA-PEDETVCXIT--EEDG 183
CY 133 YTLISVSTIVFLVMTACVSVFPAAPFGHALLVNVFHSIFVPGVCENEDEGAP 251
DB 184 VAFVAVSVSYFLFALLLMVCFVVAKE...-SFLKESSZYIERSDSQVY 233
CY 252 KKEEPCQEMNIPESLPSPRNSRNPRLPCGCCAAKVFITITSSVYSLFELAVI 311
DB 234 LEMH KQNTVDEDAIBSRTHPALBLKESREKPAKTLGIVGSEVLCWLP--FELV 290
CY 312 AVWVDVETQV QWVITIIIMFLPLOCCHPYVYGVMHTIKKEIFKPPY 370
DB 231 PLGSIFFAVPSSTVEKIFTFWLGYSRCHTPIYLSNGSEFFAPGCLL SVHGLKPTR 349
CY 371 EDSHDLPGTEGTEG-KIVPSYDSATFP 398

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Db 350 AHHH-HLSVGSQSTQGHSLTSLDSEKAP 377

RESULT 8

ID SH1A_FUGRU STANDARD; PRT; 423 AA.

AC 042385;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE 5-hydroxytryptamine 1A-alpha receptor (5-HT-1A-alpha) (Serotonin receptor) (5-HT1A-alpha) (F1A).

OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Takifugu.

OX NCBI_Taxid=31033;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RA MEDLINE=97361762; PubMed=9218723;

RT Yamaguchi F., Brenner S.;

RT "Molecular cloning of 5-hydroxytryptamine (5-HT) type 1 receptor genes from the Japanese puffer fish, Fugu rubripes.";

RL Gene 191:219-223(1997).

CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST TO THE OTHER SHT-1 SUBTYPE RECEPTORS.

CC -----

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CC -----

CC EMBL; X95936; CA65175.1; -.

CC HSSP; P29374; 1MMH.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7cm.1; 1.

DR PRINTS; PR00237; GPCRHOPOPSN.

DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.

KM G-protein coupled receptor; Transmembrane; Glycoprotein; Multi-gene family.

KM DOMAIN 1 45

FT TRANSSEM 46 71

FT DOMAIN 72 82

FT TRANSSEM 83 107

FT DOMAIN 108 118

FT TRANSSEM 119 141

FT DOMAIN 142 161

FT TRANSSEM 162 186

FT DOMAIN 188 200

FT TRANSSEM 201 226

FT DOMAIN 227 346

FT TRANSSEM 347 368

FT DOMAIN 369 379

FT TRANSSEM 380 404

FT DOMAIN 405 423

FT DISULFID 118 196

FT CARBOHYD 9

FT CARBOHYD 12 12

FT CARBOHYD 30 30

SEQUENCE 423 AA; 47000 MW; 7B1308626B40190F CRC64;

Query Match 16.7%; Score 349; DB 1; Length 423;

Best Local Similarity 27.4%; Pred. No. 2,3e-15;

Matches 106; Conservative 60; Mismatches 163; Indels 58; Gaps 10;

QY 28 LAMGIRSTVTVLFLAASFGVN--IVLALVLRKPKQLQVTFNFIPLVTDLIQISIVA 85

DB 42 LSIQITSLFLGALILCSIFGNSCVAAIALER--SLQNVANYLIGSLAVTDLVSVLV 99

QY 86 PNVATSVPLFWPLNHFCTALVSLTHLFASAVNTIVVSVDRYLSIHPLSPSKMTQ 145

DB 100 PMALVQVINKMTLGDDICDIFALDLVLCCTSSILHCAIALDRYMATIDPIDVNRKP 159

QY 146 RRGVLLVGTWIVAILQSTPPPLVGCQAPFERNALCSMTIGASPSYTIISVSFVIPL 205

DB 160 RAAAVLISVTMLIGFSISIPMLGW--RSAEDRANPDACII--SQDPGYTSTFCAFYIPL 217

QY 206 IVMACYSVPCARQHALLVNKRHSLEVRVKDCV-----ENDEBAEKKEE 255

DB 218 IMLVLYGRIFKRAAR--FRIRKTVKTEKAKASDMCLTLPSPAVFHKRANGDAVSAEMKRG 275

QY 256 FQDENMIP-----ESLPSPRRNSNMP--PIPCVQC----- 285

DB 276 YKFKSPSPCANGAVRHGEEMESLEIIEVNSNKTUPLPNTPQSSSHENINEKTTGRRK 335

QY 266 -----KAAYIFIIIFSVLSLGPYCLAVLAVWVDVETQVPQWVTITIIWLFLQCC 338

DB 336 IALAEKRTVKTLGILMGTFPCWLPFIVLALVLPFCABNCYMEWIGAVINWLGYSNSL 395

QY 339 IHPVYGYMKTIRKEIDMLKFFCK 365

DB 396 INPIYAVENKDFQSAFKILR---CK 419

RESULT 9

ID SH1A_RAT STANDARD; PRT; 422 AA.

AC 019327;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DE 15-DEC-1998 (Rel. 37, Last annotation update)

DE 5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor) (5-HT1A) OR 5HT1A.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_Taxid=10116;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=90202832; PubMed=2156831;

RA Albert P.R., Zhou Q.-Y., van Tol H.H.M., Bunzow J.R., Civelli O.;

RT "Cloning, functional expression, and mRNA tissue distribution of the rat 5-hydroxytryptamine 1A receptor gene.";

RT J. Biol. Chem. 265:5825-5832(1990).

RL [2]

RN SEQUENCE FROM N.A.

RX MEDLINE=90355775; PubMed=2167416;

RA Fujiwara Y., Nelson D.L., Kashihara K., Varga E., Roeske W.R.;

RA Yamamura H.I.;

RT "Role of cytochrome P450 in the control of the production of the erythropoietin".

RL Life Sci. 47:127-132(1990).

CC -!- FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST TO THE OTHER SHT-1 SUBTYPE RECEPTORS.

CC -----

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DR EMBL: M76446; AAB5496.1; -
DR EMBL: U03864; AAB60351.1; -
DR EMBL: L31772; AAB59487.1; -
DR EMBL: S70782; AAB31163.2; -
DR EMBL: D29952; BAAC6523.1; -
DR PIR: JH0447; JH0447.
DR Genew: HGNC:280; ADRAID.
DR MIM: 104219; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Extracellular; Lipoprotein; Palmitate.
KW Multisite family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 95
FT TRANSSEM 96 121
FT DOMAIN 122 133
FT TRANSSEM 134 159
FT DOMAIN 160 169
FT TRANSSEM 170 192
FT DOMAIN 193 213
FT TRANSSEM 214 238
FT DOMAIN 239 251
FT TRANSSEM 252 275
FT DOMAIN 276 348
FT TRANSSEM 349 373
FT DOMAIN 374 380
FT TRANSSEM 381 405
FT DOMAIN 406 572
FT LIPID 419 419
FT LIPID 422 428
FT DOMAIN 432 428
FT CONFLICT 1 83
FT FT
FT FT
FT FT
FT CONFLICT 31 31
FT CONFLICT 489 572
FT FT
FT FT
FT CONFLICT 522 522
SQ SEQUENCE 572 AA: 60462 MW: 60462 MW; EEEB134CF20A4988 CRC64;
Query Match 15.6%; Score 326.5; DB 1; Length 572;
Best Local Similarity 27.7%; Pred. No. 7.9e 14;
Matches 96; Conservative 58; Mismatches 157; Indels 35; Gaps 10;
DB 94 AAGGAGVGVFLAAFIIMAAAGNLVLSAENRHLDTVNYFVLNLAVALDLSATVLPFS 153
QY 29 AHGIIRSVLVIFLAASVGNVLALVLRKQLQVNRFLFNLVYLDLQISLVAEV 88
DB 94 AAGGAGVGVFLAAFIIMAAAGNLVLSAENRHLDTVNYFVLNLAVALDLSATVLPFS 153
QY 89 VATSVPLFMPNLSHETALVSLTHFAFASVNTIVASDRYLSIIHPISYSPKTOERG 148
DB 154 ATMEVLGFWARGACDVMADVLCGASISLCTISVDRVGVGRHGIKYPAINTERKA 213
QY 149 YLLVGTIVALLQSTPLPYLQWGQ-ALDERNALCQSMTIGASPSYTIISVSFVILIV 207
DB 214 AAILMLVWVVALVSVGLTGWKEVPPDER--FCGITEEA--GAIVFSSVCSFYLPMAV 269
QY 208 MIACSVVFCAR-RQHLLTVVRKHS-----LEVAVKDCEVNEDEGAE---KKE 254
DB 270 IVWVYCRVYVARSTTRSLKGVKRGKASVVLRIHRCGAATAD--GAHGMSAKGH 327
QY 255 EFQEDMNIPESLPSRRNSNPNPLRCYQCKAAKAVFIILFSVLSLGPYCFGLAVLAW 314
DB 328 TFPSSLSV-PLTKFSPEK-----YAAKTALIVGVFVLCMPPEFVLPLOS- 372
QY 315 VDEVGVQWVYTIITIMLFLOCCIHPIVYVYGMMTKTIKEIDMLK 360
DB 373 LPPLKPSSEGVAFKVIEMVGYFNSCVNPLIPYCSSEFFRAFLRLR 418

Query Match	Best Local Similarity	Score 325;	DB 1;	Length 416;
Matches 107;	Conservative 66;	Mismatches 174;	Indels 78;	Gaps 133;

Db 371 LKPSGVFKVIFWLGFNSCVNPILYPCSSRFPKAPFLRLR 412

RESULT 13

ID SH1A_HUMAN STANDARD; PRT; 422 AA.

AC P08908; 01-NOV-1988 (Rel. 09, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 5-hydroxytryptamine 1A receptor (5-HT_{1A}) (Serotonin receptor) (5-HT_{1A}) (G-21).

GN HT1A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RP MEDLINE=87315369; PubMed=3041227;

RA Koblika B.K., Fritelle T., Collins S., Yang-Feng T.L., Koblika T.S., Francke U., Lefkowitz R.J., Caron M.G.; "An intronless gene encoding a potential member of the family of receptors coupled to guanine nucleotide regulatory proteins."

RT Nature 329:75-79(1987).

RL Nature 335:358-360(1988).

RA Saltzman A.G., Morse B., Felder S.;

RA Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.

RP FUNCTION.

RA MEDLINE=88334700; PubMed=3138543;

RA Fargis A., Raymond J.R., Lohse M.L., Koblika B.K., Caron M.G., Lefkowitz R.J.;

RT "The genomic clone G-21 which resembles a beta-adrenergic receptor sequence encodes the 5-HT_{1A} receptor."

RL Nature 335:358-360(1988).

RP VARIANT ASP-272.

RA MEDLINE=98425601; PubMed=9754630;

RA Kawamishi Y., Harada S., Tachikawa H., Okubo T., Shiraiishi H.;

RT "Novel mutations in the promoter and coding region of the human 5-HT_{1A} receptor gene and association analysis in schizophrenia."

Am. J. Med. Genet. 81:434-439(1998).

CC FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC HORMONE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLYLATE CYCLASE ACTIVITY.

CC SUBCELLULAR LOCATION: Integral membrane protein.

CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC STRONGEST TO THE OTHER SH1-1 SUBTYPE RECEPTORS.

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EMBL, M28269; AAA6440.1;

EMBL, X13556; CAA1908.1;

EMBL, X57829; CAA0962.1;

EMBL, M83181; AAA66493.1;

PIR, S07343; S07343.

PIR, S31438; S31438.

HSSP, P29274; 1MNH.

Genew, HGNC:5286; HT1A.

MIM, 109760;

InterPro, IPR000276; GPCR_Rhodopsn.

Pfam, PF00001; 7tm_1; 1.

DR PRINTS; PRO0237; GPCRHHODPSN.

DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Polymorphism.

FT DOMAIN 1 36

FT TRANSMEM 37 62

FT DOMAIN 63 73

FT TRANSMEM 74 98

FT DOMAIN 99 109

FT TRANSMEM 110 132

FT DOMAIN 133 152

FT TRANSMEM 153 178

FT DOMAIN 179 191

FT TRANSMEM 192 217

FT DOMAIN 218 247

FT TRANSMEM 248 345

FT DOMAIN 346 367

FT TRANSMEM 368 378

FT DOMAIN 379 403

FT TRANSMEM 404 422

FT DOMAIN 423 442

FT TRANSMEM 443 462

FT CARBOHYD 463 482

FT CARBOHYD 483 502

FT DISULFID 503 522

FT VARIANT 109 187

FT VARIANT 16 16

FT VARIANT 22 22

FT VARIANT 28 28

FT VARIANT 184 184

FT VARIANT 220 220

FT VARIANT 272 272

FT VARIANT 273 273

FT CONFLICT 152 154

FT CONFLICT 172 172

FT CONFLICT 418 418

FT SEQUENCE 422 AA; 46106 MW; 762644FCF62CFDB8 CRC64;

Query Match 15.4%; Score 321.5; DB 1; Length 422;

Best Local Similarity 24.0%; Pred. No. 1.2e-13;

Matches 95; Conservative 72; Mismatches 170; Indels 59; Gaps 7;

26 ISLAHGIINSTVIVITFLASFGVN--IVLVLQKPKQLQVTRFFINLVTDLQISTL 83

31 VIVSYGVITSLTGLTIFCAVLGNACVAIAALER--SLGNVANYLGLSLAVTDLMSVL 88

84 VAPWVATSVPLFWPINSHPCTALVSLTHLFAVASVTIVVSVDRYLSIHPLSYPSKM 143

89 VLPMAALYGLVLMKMTIGQVTCDFILVDLCTSSLIHICAILDRWALTDPIDYVNR 148

144 TORRGILLIGYWIYVAILLOSTPPYLGWGAAPDERNALCSMIGASPSYITLVSFTVI 203

149 TPRRAALISLIMLIGFLISIPMLGMRP--EDREDPACTISKDHGYITVTFGAFYI 206

204 PLIVMIACYSVVFCAAR--RQHALLVNVRKHSLEVR----- 237

207 PLLMLLVYGRIFRAARFRIRKTVKVEGTGADTRHGASPADQPKSVNGSGSRWRLLG 266

238 ---VKDCYENDEGEAKKEEFODEMNIPESLP-PS-----R 270

267 VESRAGALCANGAVRQDDGALAEVIEHVRVGNKSHLPLPSEAGPTPCASFERKVB 326

271 RNSNSNPPLPRCYQCKAKVIFIIIFSVVLSGRCFLAVLAWWDVEVQDPQWVITII 330

327 RNABAKRMALAREKVTYKTIIGIMTFILCWLPFFIVALVLPFCSSGCMPTLLGAIIN 386

331 WLFFLOCCHPYYVGVNKKITKKEIQLMKKPFCKE 366

107 W09TRSLHVFVAVFHTPCRAFFIT:KCFQFQ 422

RESULT 14

CHLA MOUSE STANDARD; PRT; 421 AA.

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

5-hydroxytryptamine 1A receptor (5-HT_{1A}) (serotonin receptor) (5-HT_{1A}) OR GPCR18.

Mus musculus (Mouse).

Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

NCBI_Taxid:10090.

SEQUENCE FROM N.A.

STRAIN NIH Swiss, Tissue: Brain,

MEDLINE:34076019, Pubmed:824366;

Charest A., Malner B.H., Albert P.R.;

"Cloning and differentiation induced expression of a murine serotonin_{1A} receptor in a septal cell line";

J. Neurosci. 13:5164-5171(1993).

SEQUENCE OF 1-23 FROM N.A.

STRAIN C3H/An;

MEDLINE:36623425, Pubmed:8626733;

Palms C.L., Shenk T.;

"The serotonin 1A receptor gene contains a TATA-less promoter that responds to Maz and Sp1.";

J. Biol. Chem. 271:4417-4424(1996).

SEQUENCE OF 1-153 FROM N.A.

Tissue: Testis;

MEDLINE:9416980, Pubmed:8298218;

Winkle T.M., Chen Y., Gilbert R.J., Moore V.J., Yu L., Simon M.I., Cepeda N.G., Jenkins N.A.;

"Identification, chromosome location, and genome organization of mammalian G-protein-coupled receptors.";

Genomics 18:175-184(1993).

FUNCTION: THIS IS ONE OF THE SEVERAL DIFFERENT RECEPTORS FOR 5-HYDROXYTRYPTAMINE (SEROTONIN), A BIOGENIC AMINE THAT FUNCTIONS AS A NEUROTRANSMITTER, A HORMONE, AND A MITOGEN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY.

CELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: MOST ABUNDANTLY EXPRESSED IN MIDBRAIN AND CORTIX.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS STRONGEST TO THE OTHER 5HT-1 SUBTYPE RECEPTORS.

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EMBL: U39393; AAAA519.1;

EMBL: U39393; AAC02572.1;

EMBL: U39393; AAA16850.1;

HSSP: P29274; IMMH.

MGD: MGI:96273; Herta.

InterPro: IPR000276; GPCR_Phosphn

Pfam: PF00003; 7tm_1; 2

PRINTS: P00027; GPCRPHOSN.

PROSITE: P00027; G-PROTEIN_RECEP_F1_1; 1.

PROSITE: P00027; G-PROTEIN_RECEP_F1_2; 1.

G protein coupled receptor, Transmembrane, Glycoprotein, Multigene family.

Query Match 15.3%, Score 320.5, DB 1; Length 421;
Best Local Similarity 24.3%, Pred No. 14e-13;
Matches 98, Conservative 74, Mismatches 155, Indels 77, Gaps 12;

Query	Match	Score	DB 1	Length	421
26	ISLHGIIPSTLVVIFVFAASVFN--VLAIVIGPPDQLQVTFEIFNLVTDLQISL	83			
31	VIFSVGVITSLGLTIFCAVAGHVAVNAIALEF-SIQVAVNLISLAVTGLMVSVL	98			
84	VAPWVATVPELPFPLNHPGALVSLTHLPAPASNTIVVSVPPVLSIHPLSPSKM	143			
89	VFMALVGVLFHMTLGVCTDEFLALDVLCTSSLHCAIALCEYVWMTITIDVNR	148			
144	TSPGGLLYGTWVVALSTPPLVGMQAAPEEPA-LQSMWGAAPSYTLISVSVFT	202			
149	TFPAAATSLHWLTFSLSTITKCNPAIEDPSAPNCTT--SCHYVTITGTGAEV	205			
203	PLIVIAVYVFCAPSPGALLINVPHSLEVEV	239			
206	PLILMLVLYGPIFMAP--PIIPYVYVFFKAGTSPGSSAPPKSLNGQPG	259			
249	---EGRKEKFECEMHFE-----SLPPEPRNSNPT	279			
260	SGCGPSAENPAVTCGACAVAPQEDDATLEVTVHPVGNKSGDLPDSGATSY--V	317			
280	PCY-----GCVAAVIFIIISVYSLGPGCYCLAVIAVAVDVEGV	321			
318	PCIPKPKPTMAKPYMALAPEPTVYKGLIMGFILQWLPFIALVTPGESSCHM	377			
322	PCWVITIIIMLFPGCHHPYVGVNKKTYPRICWMLPPPY	365			
378	FELGALIMWLSYSLHNFVYAVENKPCVNAFKYIIVCPGP	421			

RESULT 15

ALAB MESAU STANDARD; PRT; 515 AA.

ID A18841;

01-NOV-1990 (Rel. 16, Created)

01-NOV-1990 (Rel. 16, Last sequence update)

15-JUN-1998 (Rel. 36, Last annotation update)

Alpha-1B adrenergic receptor (Alpha 1B-adrenoceptor)

ADRA1B.

Euteleostomi, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 11:02:50 ; Search time 83 Seconds

(without alignments)
638.961 Million cell updates/sec

Title: US-09-841-741-2

Perfect score: 2093

Sequence: 1 MTSCTNSTRESNSHTCMP.....GTGCTGCTIVPSYDATFP 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
A.Geneseq.101002:*
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2093	100.0	398	23	AAU51646
2	2024	96.7	508	22	AAU25605
3	2024	96.7	508	22	AAU25605
4	2024	96.7	508	22	AAU25605
5	2024	96.7	508	22	AAU25605
6	2024	96.7	508	22	AAU25605
7	2024	96.7	508	22	AAU25605
8	2021	96.6	508	22	AAU25605
9	2021	96.6	508	22	AAU25605
10	2019	96.5	508	22	AAU25605

11	2002	95.7	508	23	ABE07985	Human seven trans
12	1901	90.8	485	23	AAE15642	Human G-protein co
13	794	37.9	204	22	AAU25561	Human G-protein co
14	769.5	36.8	242	23	AAU69568	Human G-protein co
15	430.5	20.6	454	19	AAU58586	Human histamine H2
16	430	20.5	407	21	AAU70343	Human G-protein co
17	422.5	20.2	552	21	AAU14847	Human novel G-prot
18	409	19.5	529	17	AAU90989	Human adrenergic G
19	409	19.5	529	17	AAU90989	Human G-protein ad
20	409	19.5	529	19	AAU70501	Human adrenergic r
21	376	18.0	466	23	ABE09280	G-protein-coupled
22	376	18.0	466	23	ABE09280	Alpha 1c adrenergic
23	371.5	17.7	466	15	AAU11765	Human alpha-1C adr
24	371.5	17.7	466	15	AAU11765	Human alpha-1C adr
25	371.5	17.7	466	16	AAU90038	Human alpha-1C adr
26	371.5	17.7	466	16	AAU90038	Human alpha-1C adr
27	371.5	17.7	466	16	AAU90038	Human alpha-1C adr
28	371.5	17.7	466	22	AAU05407	Human adrenocept
29	366.5	17.5	466	22	AAU05407	Human alpha-1C3 ad
30	366.5	17.5	466	17	AAU03714	Human alpha-1C ad
31	366.5	17.5	466	15	AAU58679	Human alpha-1C ad
32	366.5	17.5	466	16	AAU58679	Human alpha-1C ad
33	366.5	17.5	466	16	AAU58679	Human alpha-1C ad
34	366.5	17.5	466	16	AAU58679	Human alpha-1C ad
35	366.5	17.5	466	21	AAU57170	Human alpha-1C ad
36	366.5	17.5	466	21	AAU57170	Human alpha-1C ad
37	366.5	17.0	466	22	AAU29934	Sequence of human
38	366.5	17.0	466	15	AAU29934	Novel human secret
39	366.5	17.0	466	15	AAU29934	Sequence of human
40	366.5	17.0	466	15	AAU29934	Novel human secret
41	366.5	17.0	466	15	AAU29934	Sequence of human
42	366.5	17.0	466	15	AAU29934	Novel human secret
43	366.5	17.0	466	15	AAU29934	Sequence of human
44	366.5	17.0	466	15	AAU29934	Novel human secret
45	366.5	17.0	466	15	AAU29934	Sequence of human

ALIGNMENTS

RESULT 1
AAU51646
ID AAU51646 standard; Protein: 398 AA.
XX
AC AAU51646;
XX
XX 19-FEB-2002 (first entry)
XX
DE Human nGPCR-2644 polypeptide.
XX
XX Human; G-protein-coupled receptor; nGPCR-2644; infection; gene therapy;
KW human immunodeficiency virus; HIV; cancer; diabetes; inflammation;
KW cardiovascular disorder; neurological disorder; rheumatoid arthritis;
XX autoimmune disorder; hormonal disorder; renal failure; psoriasis; asthma.
OS Homo sapiens.
XX
XX WO200181410-A2.
XX
XX 01-NOV-2001.
XX
XX 25-APR-2001; 2001WO-US13249.
XX
XX 25-APR-2000; 2000US-199558P.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Lind P, Sejlitz T, Vogel J;
XX WPI; 2002-041396/05.
XX N-PSDB; ABA03782.
XX
XX Novel G-protein-coupled receptor-2644 nucleic acid molecule and


```

Db 181 LCSMWGASPSYTIISVSVFIVIPLIWMIACYSVFCARROHALLYNKRHSLEVRVD 240
QY 241 CVENDEEGAEKKEEFOE----- 259
Db 241 CVENDEEGAEKKEEFOESEFRROEGEVKAKEGRMEAKDGLAKEGSTGTSESSVFA 300
QY 260 ----- 259
Db 301 RGSEEVRESSTVASDGSMEGKEGKTKVEENSMKADKGRTEVQCSDLGEDDMFGEDDI 360
QY 260 -----MNPESLPSPSRNSNSNPPLPRCYCKAKAVIIFIIIFSYVLSLGPYCFILAV 310
Db 361 NFSEDDVEAVNIPESLPSPSRNSNSNPPLPRCYCKAKAVIIFIIIFSYVLSLGPYCFILAV 420
QY 311 LAWWDVETQVPOWVITIIIMLFLOCCIHPIVYGYMHTIKKEIQDMKKPFCKEKPPK 370
Db 421 LAWWDVETQVPOWVITIIIMLFLOCCIHPIVYGYMHTIKKEIQDMKKPFCKEKPPK 480
QY 371 EDSHPDLPCTEGTEGKIIVPSYDSATFP 398
Db 481 EDSHPDLPCTEGTEGKIIVPSYDSATFP 508

RESULT 3
AAB86428
ID AAB86428 standard; Protein; 508 AA.
AC AAB86428;
DT 19-OCT-2001 (first entry)
DE Human brain SERALPHA protein.
KW SERALPHA; human; brain; G protein receptor; medicine.
XX
XX Homo sapiens.
XX DE10004930-A1.
XX PD 09-AUG-2001.
XX PF 04-FEB-2000; 2000DE-1004930.
XX PR 04-FEB-2000; 2000DE-1004930.
XX PA (BRUE/) BRUESS M.
XX PA (BOEN/) BOENISCH H.
XX PT Bruess M, Boenisch H;
XX WP1: 2001-489887/54.
XX DR N-PSDB; AAH48673.
XX

PT Gene encoding a protein of the G protein receptor super family, having
PT homology to neurotransmitter receptors is useful to develop new
PT medicaments -
PS
PS Disclosure; Page 4; 8bp; German.
XX
XX This invention describes a novel human brain-derived G protein receptor
XX gene and its encoding protein, designated SERALPHA. The receptor or cells
XX expressing the receptor are used to develop new medicines, chemicals and
XX technologies, and to devaluate existing medicines and technologies.
XX
XX Sequence 508 AA;
XX
XX Query Match 96.7%; Score 2024; DB 22; Length 508;
XX Best Local Similarity 78.1%; Pred. No. 3.8e-204;
XX Matches 397; Conservative 1; Mismatches 0; Indels 110; Gaps 1;
XX
QY 1 MTSTCTNSTPESNSHTCMPLSKMPSLHAHGIIRSTVLVIFLAASFVGNIVALTVOQRP 60
Db 1 MTSTCTNSTPESNSHTCMPLSKMPSLHAHGIIRSTVLVIFLAASFVGNIVALTVOQRP 60

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QY 61 QLLQVTRNFIENLVITDLSQISLVAPWVATSVPLPFWPLNSHPECTALVSLTHLFAFASVN 120
Db 61 QLLQVTRNFIENLVITDLSQISLVAPWVATSVPLPFWPLNSHPECTALVSLTHLFAFASVN 120
QY 121 TIVVSVDRYLSIIHPLSPSKMTORRGYLLYGTWIVAILQSTPPLYGWGAARDERNA 180
Db 121 TIVVSVDRYLSIIHPLSPSKMTORRGYLLYGTWIVAILQSTPPLYGWGAARDERNA 180
QY 181 LCSMWGASPSYTIISVSVFIVIPLIWMIACYSVFCARROHALLYNKRHSLEVRVD 240
Db 181 LCSMWGASPSYTIISVSVFIVIPLIWMIACYSVFCARROHALLYNKRHSLEVRVD 240
QY 241 CVENDEEGAEKKEEFOE----- 259
Db 241 CVENDEEGAEKKEEFOESEFRROEGEVKAKEGRMEAKDGLAKEGSTGTSESSVFA 300
QY 260 ----- 259
Db 301 RGSEEVRESSTVASDGSMEGKEGKTKVEENSMKADKGRTEVQCSDLGEDDMFGEDDI 360
QY 260 -----MNPESLPSPSRNSNSNPPLPRCYCKAKAVIIFIIIFSYVLSLGPYCFILAV 310
Db 361 NFSEDDVEAVNIPESLPSPSRNSNSNPPLPRCYCKAKAVIIFIIIFSYVLSLGPYCFILAV 420
QY 311 LAWWDVETQVPOWVITIIIMLFLOCCIHPIVYGYMHTIKKEIQDMKKPFCKEKPPK 370
Db 421 LAWWDVETQVPOWVITIIIMLFLOCCIHPIVYGYMHTIKKEIQDMKKPFCKEKPPK 480
QY 371 EDSHPDLPCTEGTEGKIIVPSYDSATFP 398
Db 481 EDSHPDLPCTEGTEGKIIVPSYDSATFP 508

RESULT 4
AAU04369
ID AAU04369 standard; Protein; 508 AA.
AC AAU04369;
DT 23-OCT-2001 (first entry)
DE Human G-protein coupled receptor, hrup15.
KW Human; G-protein coupled receptor; GPCR; hrup15; agonist;
KW inverse agonist; lung cancer.
XX
XX Homo sapiens.
XX WO200136471-A2.
XX PD 25-MAY-2001.
XX PF 16-NOV-2000; 2000WO-US31509.
XX PR 17-NOV-1999; 99US-0166088.
XX PR 17-NOV-1999; 99US-0166099.
XX PR 17-NOV-1999; 99US-0166369.
XX PR 23-DEC-1999; 98US-0171900.
XX PR 23-DEC-1999; 98US-0171901.
XX PR 11-FEB-2000; 2000US-0181749.
XX PR 14-MAR-2000; 2000US-0189258.
XX PR 14-MAR-2000; 2000US-0189259.
XX PR 10-APR-2000; 2000US-0195899.
XX PR 10-APR-2000; 2000US-0196078.
XX PR 28-APR-2000; 2000US-0200419.
XX PR 12-MAY-2000; 2000US-0203630.
XX PR 12-JUN-2000; 2000US-0210741.
XX PR 12-JUN-2000; 2000US-0210982.
XX PR 21-AUG-2000; 2000US-0226760.
XX PR 26-SEP-2000; 2000US-0235418.

```

PR 26 SEP 2000; 2000US 0235779.
 PR 20-OCT-2000; 2000US 0242332.
 PR 20 OCT 2000; 2000US 0242343.
 XX
 FA (AFEN-) APENA PHARM INC.
 XX
 PI Chen R, Dang HT, Lowitz KP;
 XX
 DR WPI: 2001-355616/37.
 DR N-PSTR; AAS07942.
 XX
 PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 XX
 PS Claim 29; Page 102-104; 160pp; English.
 XX
 CC The sequence represents a human G-protein coupled receptor (GPCR),
 CC hPRIP1. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.
 XX
 SO Sequence 508 AA;
 Query Match 96.7%; Score 2024; DB 22; Length 508;
 Best Local Similarity 78.1%; Pred. No. 3.8e-204;
 Matches 397; Conservative 1; Mismatches 0; Indels 110; Gaps 1;
 Oy 1 MTSTCTNSTRENSNHTCMPLSKMPSISLAHGIIIRSTVIVIFLAASFVGNIVATLVLOKRP 60
 Db 1 MTSTCTNSTRENSNHTCMPLSKMPSISLAHGIIIRSTVIVIFLAASFVGNIVATLVLOKRP 60
 Oy 61 QLLQVTRNFIFNLVTLTDLQISLVAPWVAVTSVPLFWMPLNSHFCALVSLTLFAFASVN 120
 Db 61 QLLQVTRNFIFNLVTLTDLQISLVAPWVAVTSVPLFWMPLNSHFCALVSLTLFAFASVN 120
 Oy 121 TIVVSVDRYLSIIHPLSYSPKMTQPRGYLLYGTVIAVILQSTPPLYGWGAADFERN 180
 Db 121 TIVVSVDRYLSIIHPLSYSPKMTQPRGYLLYGTVIAVILQSTPPLYGWGAADFERN 180
 Oy 181 LCSMTWGAASPSYTLISVSVFIVPLIWMIACTSVVFCARROHALLYNVRSLSLEVRKD 240
 Db 181 LCSMTWGAASPSYTLISVSVFIVPLIWMIACTSVVFCARROHALLYNVRSLSLEVRKD 240
 Oy 241 CVENEDGAEKKEEFODE 259
 Db 241 CVENEDGAEKKEEFODESEFRQRHEGEVAKAEGMEAKDGLKAKEGSTGTSSEV 300
 Oy 260 259
 Db 301 RGRFVRSSVYVAGSNGEKGSTKVENSMKADKGRTEVNOCSIDLGEDMEFGEDD 360
 Oy 260MNIPESLPSPRNSNSNPPLPCYCCKAAKAVIFIIISYVLSLQPYGLAV 310
 Db 361 NPSFDVEAVNIPESLPSPRNSNSNPPLPCYCCKAAKAVIFIIISYVLSLQPYGLAV 420
 Oy 311 LAWVADVETQVQWVITIIIMLFLOCCIHPIVYVYGMAKTIKKEIDMKLKKFCCKEPPK 370
 Db 421 LAWVADVETQVQWVITIIIMLFLOCCIHPIVYVYGMAKTIKKEIDMKLKKFCCKEPPK 480
 Oy 371 EDSDPDLPGTGGTGKTIVPSYDSATFP 398
 Db 481 EDSDPDLPGTGGTGKTIVPSYDSATFP 508
 RESULT 5
 AAG64126

ID AAG64126 standard; Protein; 508 AA.
 XX
 AC AAG64126;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human G protein-coupled receptor GPRV72.
 XX
 KW Human; guanosine triphosphate binding protein-coupled receptor;
 KW G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;
 KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;
 KW Alzheimer's disease; cytostatic; hepatotropic; nootropic;
 KW neuroprotective; gene therapy; peptide therapy.
 XX
 OS Homo sapiens.
 XX
 PN W0200148188-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-JF09408.
 XX
 PR 28-DEC-1999; 99JP-0375152.
 PR 31-MAR-2000; 2000JP-0101359.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M,
 PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;
 DR WPI: 2001-425662/45.
 DR N-PSDB; AAH73517.
 XX
 PT New DNA encoding guanosine triphosphate binding protein coupled
 PT receptors and their expression products for screening potential
 PT anticancer and nootropic drugs and in diagnosis of these diseases -
 XX
 PS Claim 1; Page 135-138; 170pp; Japanese.
 XX
 CC The invention relates to nine human guanosine triphosphate binding
 CC protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,
 CC GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the
 CC genes encoding them. These genes and proteins and antibodies against
 CC the protein are useful in the treatment, prevention, diagnosis and
 CC investigation of diseases associated with G protein-coupled receptors,
 CC including cancer, cirrhosis of the liver and Alzheimer's disease.
 CC The present sequence is a G protein-coupled receptor of the invention.
 XX
 SO Sequence 508 AA;
 Query Match 96.7%; Score 2024; DB 22; Length 508;
 Best Local Similarity 78.1%; Pred. No. 3.8e-204;
 Matches 397; Conservative 1; Mismatches 0; Indels 110; Gaps 1;
 Oy 1 MTSTCTNSTRENSNHTCMPLSKMPSISLAHGIIIRSTVIVIFLAASFVGNIVATLVLOKRP 60
 Db 1 MTSTCTNSTRENSNHTCMPLSKMPSISLAHGIIIRSTVIVIFLAASFVGNIVATLVLOKRP 60
 Oy 61 QLLQVTRNFIFNLVTLTDLQISLVAPWVAVTSVPLFWMPLNSHFCALVSLTLFAFASVN 120
 Db 61 QLLQVTRNFIFNLVTLTDLQISLVAPWVAVTSVPLFWMPLNSHFCALVSLTLFAFASVN 120
 Oy 121 TIVVSVDRYLSIIHPLSYSPKMTQPRGYLLYGTVIAVILQSTPPLYGWGAADFERN 180
 Db 121 TIVVSVDRYLSIIHPLSYSPKMTQPRGYLLYGTVIAVILQSTPPLYGWGAADFERN 180
 Oy 181 LCSMTWGAASPSYTLISVSVFIVPLIWMIACTSVVFCARROHALLYNVRSLSLEVRKD 240
 Db 181 LCSMTWGAASPSYTLISVSVFIVPLIWMIACTSVVFCARROHALLYNVRSLSLEVRKD 240
 Oy 241 CVENEDGAEKKEEFODE 259
 Db 241 CVENEDGAEKKEEFODESEFRQRHEGEVAKAEGMEAKDGLKAKEGSTGTSSEV 300

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QY 260 ----- 259
DB 301 RGSEVRESSTVASDGSMEKGEKSTKVEENSMKADKGRTEVNOQSIDLGEDDMERGEDDI 360
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DB 361 NFEEDVEAVNIPESLPSRRNSNSNPPLPRCYOCKAKAVIFIIIFSYVLSLGPYCFPLAV 420
QY 311 LAWVVDVETQVPOWVITIIIMLFFLOCCIHPRVYGYMKTKIKKEIQDMLKKPFCKEKPPK 370
DB 421 LAWVVDVETQVPOWVITIIIMLFFLOCCIHPRVYGYMKTKIKKEIQDMLKKPFCKEKPPK 480
QY 371 EDSDHPDLPGTEGTEGKIIVPSYDSATFP 398
DB 481 EDSDHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 6
AAU11764
ID AAU11764 standard; Protein: 508 AA.
XX
AC AAU11764;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human alpha adrenergic receptor-like GPCR.
XX
KW Human; alpha adrenergic receptor; G protein-coupled receptor;
KW GPCR; peripheral nervous system disease; central nervous system disease;
KW urinary incontinence; benign prostatic hypertrophy; infection;
KW HIV infection; human immunodeficiency virus; pain; cancer; anorexia;
KW bulimia; asthma; Parkinson's disease; obesity; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; ulcer; allergy; psychosis;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesia;
KW Huntington's disease; Tourette's syndrome.
XX
OS Homo sapiens
XX
PN MO200188126.A2.
XX
PD 22-NOV-2001.
XX
PF 11-MAY-2001; 2001MO-EP05383.
XX
PR 15-MAY-2000; 2000US-204145P.
PR 04-DEC-2000; 2000US 250505P.
XX
PA (FARB ) BAYER AG.
XX
PI Ramakrishnan S;
XX
DR N-PSDB; AAS18898, AAS18899.
XX
PT New polynucleotide, useful for treating pain, cancer, Parkinson's
PT alpha (1a) adrenergic receptor-like G-protein coupled receptor (GPCR) -
XX
PS Claim 25; Fig 3; 123pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding an alpha
CC adrenergic receptor-like G-protein coupled receptor (GPCR) polypeptide,
CC the encoded polypeptide, fragments, derivatives and allelic variants.
CC Also include are an expression vector comprising the polynucleotide,
CC a host cell containing the vector, screening for therapeutic agents which
CC decrease or increase the activity of the receptor by binding a test
CC agent to the protein and determining whether the activity is
CC decreased or increased. A modulator of the receptor is useful for treating
CC alpha adrenergic receptor-like GPCR disorder such as peripheral or
CC central nervous system disease, urinary incontinence or benign prostatic

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CC hypertrophy. The receptor, polynucleotide or modulator is useful for
CC treating disorders such as bacterial, fungi, protozoan, and viral
CC infections, particularly those caused by HIV (human immunodeficiency
CC virus), pain, cancer, anorexia, bulimia, asthma, Parkinson's diseases,
CC obesity, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcer,
CC allergy, benign prostatic hypertrophy, and psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression,
CC delirium, dementia, severe mental retardation, and dyskinesias, such as
CC Huntington's disease and Tourette's syndrome. The polynucleotide is
CC useful in diagnostic assays for detecting diseases and abnormalities or
CC susceptibility to disease and abnormalities related to the presence of
CC mutations in the gene. The protein is useful to identify test compounds
CC which may act as agonists or antagonists, and for raising antibodies
CC The present sequence is the alpha adrenergic receptor-like GPCR.
CC
XX
SQ Sequence 508 AA;
XX
Query Match 96.7%; Score 2024; DB 23; Length 508;
Best Local Similarity 78.1%; Pred. No. 3.8e-204;
Matches 397; Conservative 1; Mismatches 0; Indels 110; Gaps 1;
QY 1 MTSTCTNSTRESNSHTCMPLSKMPLSLAHGIIRSTVLVIFLASFVGNIVLALVLOKRP 60
DB 1 MTSTCTNSTRESNSHTCMPLSKMPLSLAHGIIRSTVLVIFLASFVGNIVLALVLOKRP 60
QY 61 QLLQVNTNFFINLAVTDLLOISLVAWVAVATSVPLFWPLNSHFCTALVTLHLFAFASVN 120
DB 61 QLLQVNTNFFINLAVTDLLOISLVAWVAVATSVPLFWPLNSHFCTALVTLHLFAFASVN 120
QY 121 TIVVSVVRYSIIHPLSPYPMKMTORRGYLLGTWIVAIQSTPPLTGMGQAAFDENNA 180
DB 121 TIVVSVVRYSIIHPLSPYPMKMTORRGYLLGTWIVAIQSTPPLTGMGQAAFDENNA 180
QY 181 LCSIWIGASPSYTTILSVSFYIPLIWIACYSVFCARRQHALLVNKKHSLERVYKD 240
DB 181 LCSIWIGASPSYTTILSVSFYIPLIWIACYSVFCARRQHALLVNKKHSLERVYKD 240
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QY 260 ----- 259
DB 301 RGSEVRESSTVASDGSMEKGEKSTKVEENSMKADKGRTEVNOQSIDLGEDDMERGEDDI 360
QY 260 -----NNIPESLPSRRNSNSNPPLPRCYOCKAKAVIFIIIFSYVLSLGPYCFPLAV 310
DB 361 NFEEDVEAVNIPESLPSRRNSNSNPPLPRCYOCKAKAVIFIIIFSYVLSLGPYCFPLAV 420
QY 311 LAWVVDVETQVPOWVITIIIMLFFLOCCIHPRVYGYMKTKIKKEIQDMLKKPFCKEKPPK 370
DB 421 LAWVVDVETQVPOWVITIIIMLFFLOCCIHPRVYGYMKTKIKKEIQDMLKKPFCKEKPPK 480
QY 371 EDSDHPDLPGTEGTEGKIIVPSYDSATFP 398
DB 481 EDSDHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 7
AAU04387
ID AAU04387 standard; Protein: 926 AA.
XX
AC AAU04387;
XX
DT 23-OCT-2001 (first entry)
XX
DE GPCR-Gs fusion protein, hRUP15-GS.
XX
KW G-protein coupled receptor; GPCR; hRUP15-Gs; agonist;
KW inverse agonist; lung cancer.
XX

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OS Chimeric - Homo sapiens.
 XX Chimeric - Rattus sp.
 XX WO2001364/1-A2.
 XX
 PD 25-MAY-2001.
 PF 16-MAY-2000; 2000US-0242343.
 XX
 PR 17-NOV-1999; 99US-0166098.
 PR 17-NOV-1999; 99US-0166099.
 PR 17-MAY-1999; 99US-0166363.
 PR 23-DEC-1999; 99US-0171900.
 PR 23-DEC-1999; 99US-0171901.
 PR 23-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189958.
 PR 14-MAR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0196078.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-MAR-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 29-OCT-2000; 2000US-0242332.
 PR 29-OCT-2000; 2000US-0242343.
 XX
 XX (AREN-) ARENA PHARM INC.
 XX
 PI Chen R, Dang HT, Lowitz KP;
 XX
 XX WPI: 2001-355616/37.
 DR N-PSDB; AAS08274.
 XX
 PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 PS Example 5; Page 151-154; 160pp; English.
 XX
 CC The sequence is a G-protein coupled receptor (GPCR) fusion protein,
 CC hRUP15-Gs, being the human hRUP15 fused to the rat Gs protein.
 CC The endogenous and non-endogenous, constitutively activated versions
 CC of human G-protein coupled receptors (GPCR), are useful for direct
 CC identification of candidate compounds as receptor agonists, inverse
 CC agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.
 XX
 SQ Sequence 326 AA,
 Query Match 96.7%, Score 2024; DB 22; Length 926;
 Best Local Similarity 78.1%, Pred. No. 8,5e-204,
 Matches 397, Conservative 1, Mismatches 0, Indels 110, Gaps 1;
 CY 1 MTCTTNTSTPENSNGHTMPLSKMPLSLAHGIIPTSTVTVFIILASFGVGNIVALLVLPKP 60
 DB 1 MTSICNTSRESNSSHTCMPLSKMPLSLAHGIIPTSTVTVFIILASFGVGNIVALLVLPKP 60
 CY 61 QLLAVTNPIFLMLVTLQISILVAFWVATSVPLFWPLNSHRCMLVSLTHLPAFASVN 120
 DB 61 QLLQVTKRIFLMLVTLQISILVAFWVATSVPLFWPLNSHRCMLVSLTHLPAFASVN 120
 CY 121 TIVVSVVPIVPISTIHPLSYPSKMTQTPVYLLVGTWIVAILQSTPLPYGMQAAFDPRNA 180
 DB 121 TIVVSVVPIVPISTIHPLSYPSKMTQTPVYLLVGTWIVAILQSTPLPYGMQAAFDPRNA 180

QY 181 LGSNMGASPSYTLISVSEFIVIPLIWIAICYSVFPQAPQHALLVNVPHSLVPPVKD 240
 DB 181 LGSNMGASPSYTLISVSEFIVIPLIWIAICYSVFPQAPQHALLVNVPHSLVPPVKD 240
 QY 241 CVENDEEGAEKKEEFODE----- 259
 DB 241 CVENDEEGAEKKEEFODEEFPPCHGEVAVAPPEPPEAKFDGSLIPEEGGCTGSESVFA 300
 QY 260 ----- 259
 DB 301 KGESEVNESTVASDSMEKKESTIVVENSMWAPPTPTVPCCTITPGRDDMERGGDDI 360
 QY 260 -----MNIPESLPSPNSNSNPPLPPCYCCAKAVIFIIIFSYVLSGPPYFLAV 310
 DB 361 NPEEDVEAVNIPPSPPSPNSNSNPPLPPCYCCAKAVIFIIIFSYVLSGPPYFLAV 420
 QY 311 LAVWVDETQVQVWVITIIIMLFLOCCIHRYVYVGMKTIKKEICMLKKEFCYKPPK 370
 DB 421 LAVWVDETQVQVWVITIIIMLFLOCCIHRYVYVGMKTIKKEICMLKKEFCYKPPK 480
 QY 371 EDSHPDLPTGEGTEGKIYPSYSATFP 398
 DB 481 EDSHPDLPTGEGTEGKIYPSYSATFP 508
 RESULT 8
 ID AAB61982 standard; Protein; 508 AA.
 XX AAB61982:
 XX
 XX 14-MAY-2001 (first entry)
 XX
 DE Human G-protein coupled receptor, IGSL.
 XX
 KM G-protein coupled receptor, IGSL; psychiatric; central nervous system;
 KM movement disorder; tremor; Tourette's syndrome; Parkinson's disease;
 KM Huntington's disease; dyskinesia; dystonia; spasm; neuroleptic; human;
 KM neurotoxic; anticonvulsant; relaxant; vaccine; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200109184-A1.
 XX
 PD 08-FEB-2001.
 XX
 PF 17-JUL-2000; 2000WO-EP06878.
 XX
 PR 15-JUL-1999; 99EP-0202326.
 PR 15-JUL-1999; 99RL-1012611.
 XX
 PA (SOLV) SOLVAY PHARM BV.
 XX
 PI Deleersnijder W, Nys G, Zhang F;
 XX
 XX WPI: 2001-382942/18.
 DR N-PSDB; AAF56818.
 XX
 PT Novel human G-protein coupled receptor family polypeptide, IGSL, useful
 PT for treating psychiatric and central nervous system disorders such as
 PT tics, tremor, Tourette's syndrome and Parkinson's disease -
 XX
 XX
 PS Claim 15; Page 7; 65pp; English.
 XX
 CC This represents a G-protein coupled receptor family polypeptide, IGSL.
 CC The IGSL protein can be expressed by standard recombinant methodology.
 CC IGSL is useful for inducing immunological response in a mammal, as
 CC vaccine. IGSL polynucleotides and polypeptides and its modulators are
 CC useful for treating psychiatric and central nervous system disorders
 CC especially movement disorders, such as tics, tremor, Tourette's syndrome,
 CC Parkinson's disease, Huntington's disease, dyskinesias, dystonia and
 CC spasms

XX Sequence 508 AA;
 SQ Query Match 96.6%; Score 2021; DB 22; Length 508;
 Best Local Similarity 78.0%; Pred. No. 7.8e-204;
 Matches 396; Conservative 2; Mismatches 0; Indels 110; Gaps 1;

QY 1 MTSTCTNSTRESNSSHCTMPLSKMPLSLAHGIIRSTVVIPLAASFVGNIVATLQORXP 60
 DB 1 MTSTCTNSTRESNSSHCTMPLSKMPLSLAHGIIRSTVVIPLAASFVGNIVATLQORXP 60
 QY 61 QLLQVYTNRFIFNLVLTDLQISLVA PWVAVTSVPLFWPLNSHFCALVSLTHLPAFASVN 120
 DB 61 QLLQVYTNRFIFNLVLTDLQISLVA PWVAVTSVPLFWPLNSHFCALVSLTHLPAFASVN 120
 QY 121 TIVVSVDRYLSIHPPLSPSKMTORRGYLLYGTWIVAILQSTPPLVGMGQAARDERNA 180
 DB 121 TIVVSVDRYLSIHPPLSPSKMTORRGYLLYGTWIVAILQSTPPLVGMGQAARDERNA 180
 QY 181 LCSMTWGSASPSYTIISVSVFIVPLIWMACYSVFCARROHALLYNKRHSLERVVD 240
 DB 181 LCSMTWGSASPSYTIISVSVFIVPLIWMACYSVFCARROHALLYNKRHSLERVVD 240
 QY 241 CVENDEBGAEEKKEEFODESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA 259
 DB 241 CVENDEBGAEEKKEEFODESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA 259
 QY 260 -----MNIPESLPSPRRNSNSNPPLPRCYOCKAAKAVIFIIIFSVYLSIGPYCFLAV 310
 DB 260 -----MNIPESLPSPRRNSNSNPPLPRCYOCKAAKAVIFIIIFSVYLSIGPYCFLAV 310
 QY 361 NFSEDDVEAVNIPELSPRRNSNSNPPLPRCYOCKAAKAVIFIIIFSVYLSIGPYCFLAV 420
 DB 361 NFSEDDVEAVNIPELSPRRNSNSNPPLPRCYOCKAAKAVIFIIIFSVYLSIGPYCFLAV 420
 QY 371 EDSPHDLPGTEGTEGKIIVPSYDSATFP 398
 DB 371 EDSPHDLPGTEGTEGKIIVPSYDSATFP 398
 QY 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
 DB 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 9
 ABB75712
 ID ABB75712 standard; Protein; 508 AA.
 AC ABB75712;
 DT 24-JUN-2002 (first entry)
 DE G-protein coupled receptor AXOR69.
 KW G-protein coupled receptor; receptor; AXOR69; human; anti-HIV;
 KW virocidine; antimicrobial; analgesic; cytosolic; antidiabetic;
 KW anorectic; anabolic; antisthmatic; antiparkinsonian; cardiant;
 KW cerebroprotective; hypotensive; hypertensive; antitumor;
 KW antisthmatic; antiallergic; antileptic; tranquilizer; neuroleptic;
 KW nootropic; anticonvulsant; vaccine.
 OS Homo sapiens.
 XX GR2367295-A.
 XX 03-APR-2002.
 XX 12-JUN-2001; 2001GB-00:4287.
 XX 16-JUN-2000; 2000US-0596400.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA

PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Elshourbagy N, Gatu M, Shabon U;
 XX WPI; 2002-294789/34.
 DR N-PSDB; ABL53719.
 PT An isolated human G-protein coupled (7TM) receptor AXOR 69 polypeptide,
 PT for treating diseases such as obesity, stroke and anxiety.
 PS Claim 1; Page 27; 34pp; English.
 XX The present sequence is that of human AXOR69, a G-protein coupled
 CC receptor (GPCR) that shows homology to other members of the GPCR
 CC family, such as human adrenergic alpha-1a receptor. The invention
 CC provides AXOR69 polypeptides and polynucleotides, and methods for
 CC producing such polypeptides by recombinant techniques. Also
 CC provided are methods for using the AXOR69 polypeptides and
 CC polynucleotides to screen for compounds that stimulate or inhibit
 CC AXOR69 levels or activity. The polypeptides, polynucleotides,
 CC agonists and antagonists are used to treat conditions associated
 CC with AXOR69 imbalance, including bacterial, fungal, protozoan and
 CC viral infections, particularly HIV-1 and HIV-2 infections, pain,
 CC cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's
 CC disease, acute heart failure, hypotension, hypertension, urinary
 CC retention, osteoporosis, angina pectoris, myocardial infarction,
 CC stroke, ulcers, asthma, allergies, benign prostatic hypertrophy,
 CC migraine, vomiting, psychotic and neurological disorders, including
 CC anxiety, schizophrenia, manic depression, depression, delirium,
 CC dementia and severe mental retardation, and dyskinesias such as
 CC Huntington's disease and Gilles de la Tourette syndrome. AXOR69
 CC polypeptides are also useful in vaccines, and for raising specific
 CC antibodies.

SQ Sequence 508 AA;
 Query Match 96.6%; Score 2021; DB 23; Length 508;
 Best Local Similarity 78.0%; Pred. No. 7.8e-204;
 Matches 396; Conservative 2; Mismatches 0; Indels 110; Gaps 1;

QY 1 MTSTCTNSTRESNSSHCTMPLSKMPLSLAHGIIRSTVVIPLAASFVGNIVATLQORXP 60
 DB 1 MTSTCTNSTRESNSSHCTMPLSKMPLSLAHGIIRSTVVIPLAASFVGNIVATLQORXP 60
 QY 61 QLLQVYTNRFIFNLVLTDLQISLVA PWVAVTSVPLFWPLNSHFCALVSLTHLPAFASVN 120
 DB 61 QLLQVYTNRFIFNLVLTDLQISLVA PWVAVTSVPLFWPLNSHFCALVSLTHLPAFASVN 120
 QY 121 TIVVSVDRYLSIHPPLSPSKMTORRGYLLYGTWIVAILQSTPPLVGMGQAARDERNA 180
 DB 121 TIVVSVDRYLSIHPPLSPSKMTORRGYLLYGTWIVAILQSTPPLVGMGQAARDERNA 180
 QY 181 LCSMTWGSASPSYTIISVSVFIVPLIWMACYSVFCARROHALLYNKRHSLERVVD 240
 DB 181 LCSMTWGSASPSYTIISVSVFIVPLIWMACYSVFCARROHALLYNKRHSLERVVD 240
 QY 241 CVENDEBGAEEKKEEFODESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA 259
 DB 241 CVENDEBGAEEKKEEFODESEFRROHEGEVKAKEGRMEAKDGLKAKEGSTGTSESSVEA 259
 QY 260 -----MNIPESLPSPRRNSNSNPPLPRCYOCKAAKAVIFIIIFSVYLSIGPYCFLAV 310
 DB 260 -----MNIPESLPSPRRNSNSNPPLPRCYOCKAAKAVIFIIIFSVYLSIGPYCFLAV 310
 QY 361 NFSEDDVEAVNIPELSPRRNSNSNPPLPRCYOCKAAKAVIFIIIFSVYLSIGPYCFLAV 420
 DB 361 NFSEDDVEAVNIPELSPRRNSNSNPPLPRCYOCKAAKAVIFIIIFSVYLSIGPYCFLAV 420
 QY 371 EDSPHDLPGTEGTEGKIIVPSYDSATFP 398
 DB 371 EDSPHDLPGTEGTEGKIIVPSYDSATFP 398

|||||
441 EDSPDLPDLSIGISGKIVPSYLSATFP 508

RESULT 10
AA04384
ID AA04384 standard; Protein, 508 AA.

XX AA04384;
XX 23-OCT-2001 (first entry)

XX Human G-protein coupled receptor, hRUP15, mutant A398K.

XX HRP15, G-protein coupled receptor, GPCR, hRUP15, agonist,
XX inverse agonist; lung cancer; A398K; mutant; mulein.

XX Homo sapiens.

XX W0200136471-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000US-0241509.

XX 17-NOV-1999; 99US-0166088

XX 17-NOV-1999; 99US-0166099.

XX 17-NOV-1999; 99US-0166169.

XX 23-DEC-1999; 99US-0171900.

XX 23-DEC-1999; 99US-0171901.

XX 11-FEB-2000; 2000US-0181749.

XX 14-MAR-2000; 2000US-0189258.

XX 14-MAR-2000; 2000US-0189259.

XX 13-APR-2000; 2000US-0196898.

XX 10-APR-2000; 2000US-0196899.

XX 10-APR-2000; 2000US-0196878.

XX 28-APR-2000; 2000US-0200419.

XX 12-MAY-2000; 2000US-0203630.

XX 12-JUN-2000; 2000US-0210741.

XX 12-JUN-2000; 2000US-0210982.

XX 21-AUG-2000; 2000US-0226760.

XX 26-SEP-2000; 2000US-0236418.

XX 26-SEP-2000; 2000US-0236779.

XX 20-OCT-2000; 2000US-0242332.

XX 20-OCT-2000; 2000US-0242343.

XX (AREN) ARENA PHARM INC.

XX Chen P, Dang HT, Lowitz KP;

XX WPI; 2001-355616/37.

XX N FECS, AAG08265.

XX

XX

Claim 30, Page 141, 160PF, English.

The sequence is a human G-protein coupled receptor (GPCR), hRUP15, mutant A398K. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system. Incorporating GPCRs can be utilized to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.

Sequence 508 AA;

Query Match 96.5%, Score 2019, DB 22; Length 508;
Best Local Similarity 78.0%, Fred. No. 1.3e+203;
Matches 396; Conservative 1; Mismatches 1; Indels 110; Gaps 1;

QY 1 MTSTCTNSTRESNSSHCTMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLRKP 60
DE 1 MTSTCTNSTRESNSSHCTMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLRKP 60
QY 61 OLLQVTRPFIFNLVTDLLQSLVAPWVATSVPLFWPLNSHFCALVSLTLFPAFASVN 120
DE 61 OLLQVTRPFIFNLVTDLLQSLVAPWVATSVPLFWPLNSHFCALVSLTLFPAFASVN 120
QY 121 TIVVSVDPVYSIIHPLSPSPKTPQPGYLLYGTWVAIIQSTDPPLVGMVQAADFEDNA 180
DE 121 TIVVSVDPVYSIIHPLSPSPKTPQPGYLLYGTWVAIIQSTDPPLVGMVQAADFEDNA 180
QY 181 LCSMTWGSFSTYITLSVSVFIVPIIWMIAQSVFCARPHALLVNRKSLERVD 240
DE 181 LCSMTWGSFSTYITLSVSVFIVPIIWMIAQSVFCARPHALLVNRKSLERVD 240
QY 241 CVENDEEGAEKKEFEODE----- 259
DE 241 CVENDEEGAEKKEFEODE----- 259
QY 260 ----- 259
DE 301 PGSEFVEESTVADSGMEGKESTVEENSVKAPVPTVENQSTPLVPTFMEREPDNI 360
QY 260 ----- 310
DE 361 NFSEPDVAWNPESLPFSRNSNPNPLPCYCGKAAVFIIFESVYLSGPGCLAV 420
QY 311 LAWVAVDFEQVQWVITIIIMLFQCCIHFPVGYMHTIKKEIQGMLKPFCEYEPK 370
DE 421 LAWVAVDFEQVQWVITIIIMLFQCCIHFPVGYMHTIKKEIQGMLKPFCEYEPK 480
QY 371 EDSPDLPDLSIGISGKIVPSYLSATFP 398
DE 481 EDSPDLPDLSIGISGKIVPSYLSATFP 508

RESULT 11

ABB07985
ID ABB07985 standard; Protein, 508 AA.

XX ABB07985;

XX 12-AUG-2002 (first entry)

XX Human seven transmembrane receptor, 65499 protein.

XX Human; seven transmembrane domain receptor; 65499; 58875; cytostatic;
XX osteopathic; vasotropic; cardiac; antipsychotic; antihypertensive;
XX neuroprotective; antiparkinsonian; antidiabetic; virucide; analgesic;
XX antitubercular; antitubercular; anesthetic; immunomodulator; gene therapy

XX Homo sapiens.

XX W0200228901-A2

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US31250.

XX 05-OCT-2000; 2000US-037700P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Gluckmann MA;

XX WPI; 2002-444096/47.

XX N-PSDB; ABL41163, ABL41164.

epilepsy, Parkinson's disease, dementia, Alzheimer's disease), autoimmune
 inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple
 sclerosis), cardiovascular disorder (atherosclerosis, angina pectoris),
 gastroenteric disorder (ulcer, cholelithiasis, gastroenteritis),
 metabolic disorders (diabetes), viral infections (herpes virus) and in
 the assessment of the effects of exogenous compounds on the expression
 of the nucleic acid and amino acid sequences. The present sequence is
 human GPCR 12 protein.

Sequence 485 AA:

Query Match 99.8%, Score 1901, DB 23, Length 485,
 Best Local Similarity 77.1%, Pred. No. 3,20-191,
 Matches 374; Conservative 1; Mismatches 0; Indels 110; Gaps 1;

Db 1 MISTAHGIRPSTVIVFLAASGVNIVLALVGRPGICLVNTPTFLVTDLIQISL 63
 24 MISLAHGIRPSTVIVFLAASGVNIVLALVGRPGICLVNTPTFLVTDLIQISL 63
 1 MISTAHGIRPSTVIVFLAASGVNIVLALVGRPGICLVNTPTFLVTDLIQISL 63
 Db 94 VAPWVATSVPLFWPLNSHCTALVSLTLFAPASVNTIVVSVDEYSLSIHLSYFSK 143
 61 VAPWVATSVPLFWPLNSHCTALVSLTLFAPASVNTIVVSVDEYSLSIHLSYFSK 120
 Db 144 TORRGILLVGVIVVLIISSTPLVGMGQAAPDERNALCSMIWGASPSYTIISVSFI 203
 121 TORRGILLVGVIVVLIISSTPLVGMGQAAPDERNALCSMIWGASPSYTIISVSFI 180
 Db 204 FLIVVACSVVECAAPRGHALLVYVPHSTFVYVDYENDEEFAEYKEEPPDE 259
 181 FLIVVACSVVECAAPRGHALLVYVPHSTFVYVDYENDEEFAEYKEEPPDE 240
 Db 260 FLIVVACSVVECAAPRGHALLVYVPHSTFVYVDYENDEEFAEYKEEPPDE 259
 260 FLIVVACSVVECAAPRGHALLVYVPHSTFVYVDYENDEEFAEYKEEPPDE 259
 Db 241 PCHREVVAFPEMFAVPGSLAAEESTTSESVAFSSSEVFESSTVASQWGEFEG 300
 260 PCHREVVAFPEMFAVPGSLAAEESTTSESVAFSSSEVFESSTVASQWGEFEG 300
 Db 301 STRVEENSKAKGRTENVQCSIDLGEDMEGECDCINSEDDVEAVNIPESLPSRRNS 360
 274 NENPLFECCGCAAAVAVIIFSVYLSLGFYCFGLAVLAWVQVQVQVQVITIMF 333
 361 NENPLFECCGCAAAVAVIIFSVYLSLGFYCFGLAVLAWVQVQVQVQVITIMF 420
 Db 334 FLQCTTHPVVGVYMKTYETIQDKLYKFPCKEKPPEYSHPLPCTEGCTEKIVPSYD 393
 421 FLQCTTHPVVGVYMKTYETIQDKLYKFPCKEKPPEYSHPLPCTEGCTEKIVPSYD 480
 Db 394 SATFP 398
 481 SATFP 485

RESULT 13
 AAU25561
 ID AAU25561 standard, Protein, 204 AA.

XX AAU25561;
 18-DEC-2001 (first entry)

DE Human G Protein-coupled Receptor (GPCR) polypeptide #8.
 XX
 XX Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;
 XX attention deficit disorder; anxiety; depression; bipolar disorder;
 XX neurological disorder; Huntington's disease; dementia; obesity; anorexia;
 XX metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;
 XX type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;
 XX cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;
 XX viral infection; immunosupplant; neuroleptic; nootropic; tranquiliser;
 XX antidepressant; anorectic; gene therapy.
 XX Homo sapiens.

PN W0200162797 A2.
 XX 30-AUG-2001.
 XX
 XX 03-FEB-2001; 2001WO-US05676.
 XX
 XX 03-FEB-2000; 2000US-0184247.
 XX 03-FEB-2000; 2000US-0184303.
 XX 03-FEB-2000; 2000US-0184304.
 XX 03-FEB-2000; 2000US-0184305.
 XX 03-FEB-2000; 2000US-0184397.
 XX 03-MAR-2000; 2000US-0186457.
 XX 03-MAR-2000; 2000US-0186810.
 XX 09-MAR-2000; 2000US-0188064.
 XX 13-MAR-2000; 2000US-0188880.
 XX 03-APR-2000; 2000US-0194344.
 XX 23-JUN-2000; 2000US-0213861.
 XX 11-JUL-2000; 2000US-0217369.
 XX 14-JUL-2000; 2000US-0217370.
 XX 20-JUL-2000; 2000US-0218492.
 XX
 XX (PHMA) PHARMACIA & UPJOHN CO.
 XX
 XX Vogeli G, Wood LS, Parodi LA, Lind P;
 XX WPI; 2001-570628/64.
 XX R-FEDB; AAS42813.
 XX
 XX New isolated nucleic acid encoding a new G-protein coupled receptor
 XX polypeptide for detecting receptor modulators that can treat mental
 XX disorders, such as schizophrenia, anxiety, depression, or obesity.
 XX
 XX claim 15; Page 73; 279pp; English

XX
 XX Sequences AAU25554-AAU25616 represent human G-protein coupled receptor
 XX (GPCR) polypeptides of the invention. The proteins and their associated
 XX DNA sequences can be used to identify compounds which bind to GPCR.
 XX polypeptides and in screening for compounds that modulate GPCR activity.
 XX By screening a human subject for the presence of mutations in GPCR DNA, a
 XX GPCR-related disorder or a genetic predisposition can be diagnosed. The
 XX sequences can also be used for treatment and prevention of mental
 XX disorders such as schizophrenia, attention deficit disorder, anxiety,
 XX depression, dementia and bipolar disorder, neurological disorders such as
 XX Huntington's disease, Parkinson's disease and Tourette's syndrome,
 XX metabolic disorders such as obesity, anorexia and type 2 diabetes,
 XX cardiovascular disorders such as thrombosis, myocardial infarction,
 XX cardiomyopathy and atherosclerosis, viral infections caused by HIV and
 XX cancers.

XX
 XX Sequence 204 AA:

Query Match 37.9%; Score 794; DB 22; Length 204;
 Best Local Similarity 99.4%; Pred. No. 3,70-75;
 Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX
 XX 1 MISTCTNSTRESNSHTCPUSKMPISLAHGIIRSTVIVFLAASVGNIVLALVGRP 60
 XX 47 MISTCTNSTRESNSHTCPUSKMPISLAHGIIRSTVIVFLAASVGNIVLALVGRP 106
 Db 61 QLLQVTPPIFENLVITDQISLVAPWVATSVPLFWPLNSHCTALVSLTLFAPASV 120
 107 QLLQVTPPIFENLVITDQISLVAPWVATSVPLFWPLNSHCTALVSLTLFAPASV 166
 Db 121 TIVVSVDEYSLSIHLSYFSK 158
 167 TIVVSVDEYSLSIHLSYFSK 204

RESULT 14
 AAU69568
 ID AAU69568 standard, Protein, 242 AA.

AC AAV69568;
 XX
 DT 30-JAN-2002 (first entry)
 XX
 DE Human G protein-coupled receptor from cDNA Seq-2644.
 XX
 KW Human; G protein-coupled receptor; nGPCR; cancer; tumour;
 KW thyroid disorder; myxoedema; renal failure; inflammatory condition;
 KW Crohn's disease; cell differentiation disease; homeostasis disease;
 KW rheumatoid arthritis; autoimmune disorder; movement disorder;
 KW central nervous system disorder; stroke; Huntington's disease;
 KW Tourette's syndrome; Parkinson's disease; Alzheimer's disease;
 KW viral infection; HIV-1; HIV-2; human immunodeficiency virus;
 KW metabolic disease; cardiovascular disease; type 2 diabetes; obesity;
 KW hypertension; thrombosis; myocardial infarction;
 KW atherosclerosis; proliferative disease; hyperproliferative disorder;
 KW psoriasis; hormonal disorder; polycystic ovarian syndrome;
 KW alopecia; sexual dysfunction; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN W0200177330-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-US11330.
 XX
 PR 06-APR-2000; 2000US-195093P.
 PR 06-APR-2000; 2000US-195098P.
 PR 06-APR-2000; 2000US-195099P.
 PR 06-APR-2000; 2000US-195148P.
 PR 06-APR-2000; 2000US-195150P.
 PR 06-APR-2000; 2000US-195151P.
 PR 05-SEP-2000; 2000US-230149P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogel G;
 XX
 DR WPI; 2002-010912/01.
 DR N-PSDB; AAS62900.
 XX
 PT Novel isolated nucleic acid molecule encoding G protein-coupled
 PT receptor polypeptide, nGPCR-x, useful for treating cancer, Crohn's
 PT disease, rheumatoid arthritis, Alzheimer's disease, stroke, thrombosis,
 PT psoriasis -
 XX
 PS Claim 31; Page 80; 189pp; English.

CC rheumatoid arthritis, autoimmune disorders, movement disorders, central
 CC nervous system disorders (e.g., stroke, Huntington's disease, Tourette's
 CC Syndrome, Parkinson's disease, Alzheimer's disease), infections, such as
 CC viral infections caused by HIV-1 or HIV-2 (human immunodeficiency
 CC virus, metabolic and cardiovascular diseases and disorders (e.g., type
 CC 2 diabetes, obesity, hypertension, hyperextension, thrombosis, myocardial
 CC infarction, atherosclerosis), proliferative diseases and cancers,
 CC hyperproliferative disorders (such as psoriasis), hormonal disorders
 CC (e.g., polycystic ovarian syndrome, alopecia), and sexual dysfunction.
 CC The present sequence represents an n-GPCR of the invention.
 XX
 SQ Sequence 242 AA;
 XX
 QY Query Match 36.8%; Score 769.5; DB 23; Length 242;
 QY Best Local Similarity 81.5%; Pred. No. 1.0e-72;
 DB Matches 145; Conservative 7; Mismatches 19; Indels 7; Gaps 2;
 QY 228 NVYRHSLEVVKDC---VENEDEGAKEKEFODE---NNIPESLPSPRRNSNPPLP 280
 DB 4 SMKADKRTENVQCSIDLGEDDMFGEEDINFSDDVEAVNIPESLPSPRRNSNPPLP 63
 QY 281 RCTQCKAAKVIPIIIISYVSLGPRYFLAVLAWVDVETQVPQWVITIIIMLFFLOCCIH 340
 DB 64 RCYQCKAAKVIPIIIISYVSLGPRYFLAVLAWVDVETQVPQWVITIIIMLFFLOCCIH 123
 QY 341 PYYGYVWHKTIKKETIDMLKKPFCKEKPREDSDHDLPGTEGSGEGKIVPSYDSATFP 398
 DB 124 PYYGYVWHKTIKKETIDMLKKPFCKEKPREDSDHDLPGTEGSGEGKIVPSYDSATFP 181
 XX
 RESULT 15
 AAMS5856
 ID AAMS5856 standard; Protein; 454 AA.
 XX
 AC AAMS5856;
 XX
 DT 07-SEP-1998 (first entry)
 XX
 DE Human histamine H2 receptor.
 XX
 KW Human; histamine H2 receptor; H2RH, inflammatory disease, gastric,
 KW nervous condition.
 XX
 OS Homo sapiens.
 XX
 PN W09820040-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 05-NOV-1997; 97WO-US20200.
 XX
 PR 07-NOV-1996; 96US-0748485.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Au-Young J, Goli SK, Guejler KJ, Murry LE;
 XX
 DR WPI; 1998-286870/25.
 DR N-PSDB; AAV37701.
 XX
 PT Histamine H2 receptor - used to treat inflammatory disease, gastric
 PT conditions and nervous conditions
 XX
 Claim 1; Page 51-52; 77pp; English.

CC The present sequence represents histamine H2 receptor (H2RH) isolated
 CC from Incyte Clone 1722180 from the human bladder cDNA library
 CC (BLANOT06). A host cell, comprising a vector which contains the nucleic
 CC acid encoding H2RH, can be used to produce the H2RH. An antibody which
 CC specifically binds the H2RH can be used to detect and quantify H2RH in
 CC a biological sample. An antagonist which specifically binds to and
 CC modulates the activity of H2RH can be used in a pharmaceutical
 CC composition for treating inflammatory disease, gastric conditions, and

nerous conditions. The gastric conditions that can be treated using the antacid, include gastritis, flu, colitis, and Crohn's disease. The nervous conditions include Alzheimer's disease, ataxia, Eaton-Lambert syndrome, epilepsy, myasthenia gravis, and Parkinson's disease. The antacid may also be used to treat infections or inflammation of the urinary tract and bladder. It may also be used to modulate H2HP activity in endothelial cells of the cardiovascular system and treat diseases such as arteriosclerosis, cardiomyopathy, endocarditis, and ischaemia.

XX Sequence 454 AA:

Query March 20.6%; Score 430.5; DB 19; Length 454;

Best Local Similarity 29.2%; Pred. No. 2.1e-36;

Matches 99; Conservative 68; Mismatches 137; Indels 35; Gaps 8;

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QY 31 GIIKSTVIVIFLAASEV--GNIVLALVLRKPKQLQVTRFIFNLVTDLQISLVAPWV 88
DB 25 GVITTFQIAIVITIFVCTIGNLVIVVTLTKKSYLLTSLNKFVSLTSLNPLSLVLPFV 84
QY 89 VATSVPLFPLNSHFCALVSLTHLFAPASVNTIVVSVDPYLSIHPISYPSKMTQRCG 148
DB 85 VTSSIRREWIFGVWQCNFSALLYLILSSASMLTGVIAIDRYAVLYPMVYEMKITGNPA 144
QY 149 YLLYGTWIVALOSTPLYGWGOAFADEKRNALCSMTWGAPEYTLISVYSFIVIPLIW 208
DB 145 VMAIVYIWLHSLIGCLPPLFGSSVEFDEKMMCVAAHREPGYIAFWQIWCALPPLVM 204
QY 209 IACYSVVECTAAPFGHALLVNVYFPHSLFVYVQVEENFECAEKEEFODEMNIPESLFP 268
DB 205 LVGYGFITPVAP-----VKAPKHGCTIVIVVEDAQPTGVPHNS-----STSTSSSG 261
QY 269 SPVNS-----NSNPPLPCGYOCKAKAVIFIIISYVLSLGPY-CFLAVLAVW--VDVET 319
DB 252 SPRNAFGGVVVSAN-----OCKALITLVLGAFVTVGWGPYMWVIVASEALWGSVSP 304
QY 320 QVPQWVILIIIMLEFLQCCIHPRVYGYMKTKKEIQDM 358
DB 305 SLETTA---TWLSPASAVCHPLIYGLMKNKTVRKELDGM 339

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Search completed: February 11, 2003, 11:08:12
Job time : 86 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2003, 11:06:45 ; Search time 30 Seconds
(without alignments)
390.344 Million cell updates/sec

Title: US-09-841-741-2

Perfect score: 2093
Sequence: 1 MTSTCTNSTRESNSSHCTMP.....GTCTGTGKIVPSYDANTEP 398

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430.5	20.6	454	2	US-08-748-485-1
2	409	19.5	529	2	US-08-467-568-2
3	409	19.5	529	2	US-09-030-582-2
4	409	19.5	529	5	PCT-US94-09051-2
5	371.5	17.7	466	1	US-08-334-698-6
6	371.5	17.7	466	1	US-08-228-932-6
7	371.5	17.7	466	1	US-08-468-939-6
8	371.5	17.7	466	1	US-08-722-001-28
9	371.5	17.7	466	2	US-08-406-855A-6
10	371.5	17.7	466	2	US-08-722-190-6
11	371.5	17.7	466	3	US-08-244-354-6
12	371.5	17.7	466	4	US-09-206-899-6
13	371.5	17.7	466	4	US-09-444-783-6
14	371.5	17.7	466	4	US-09-688-415-6
15	371.5	17.7	466	4	PCT-US95-04203-6
16	366.5	17.5	429	2	US-08-748-485-7
17	366.5	17.5	466	2	US-08-722-001-12
18	366.5	17.5	466	2	US-08-467-568-11
19	366.5	17.5	466	2	US-09-030-582-11
20	355.5	17.0	466	4	US-09-688-415-11
21	355.5	17.0	466	4	US-08-406-855A-23
22	355.5	17.0	466	3	US-09-206-899-23
23	333.5	15.9	375	5	US-08-118-270-17
24	333.5	15.9	375	5	PCT-US93-08528-17
25	326.5	15.6	501	2	US-08-722-001-14
26	326.5	15.6	501	2	US-08-467-568-9
27	326.5	15.6	501	2	US-09-030-582-9

28	326.5	15.6	572	1	US-08-334-698-2	Sequence 2, Appl1
29	326.5	15.6	572	1	US-08-728-932-2	Sequence 2, Appl1
30	326.5	15.6	572	1	US-08-468-939-2	Sequence 2, Appl1
31	326.5	15.6	572	2	US-08-722-001-30	Sequence 30, Appl1
32	326.5	15.6	572	2	US-08-406-855A-2	Sequence 2, Appl1
33	326.5	15.6	572	2	US-08-722-190-2	Sequence 2, Appl1
34	326.5	15.6	572	3	US-08-244-354-2	Sequence 2, Appl1
35	326.5	15.6	572	3	US-09-206-899-2	Sequence 2, Appl1
36	326.5	15.6	572	4	US-09-444-783-2	Sequence 2, Appl1
37	326.5	15.6	572	4	PCT-US95-04203-2	Sequence 2, Appl1
38	326.5	15.6	572	5	US-07-817-920-3	Sequence 2, Appl1
39	324.5	15.5	422	1	US-08-370-542-3	Sequence 3, Appl1
40	324.5	15.5	422	1	US-08-117-006-3	Sequence 3, Appl1
41	324.5	15.5	422	1	US-08-216-594-3	Sequence 3, Appl1
42	324.5	15.5	422	2	US-08-542-358-3	Sequence 3, Appl1
43	324.5	15.5	422	2	US-08-157-185-13	Sequence 13, Appl1
44	324.5	15.5	422	3	US-08-281-526B-13	Sequence 13, Appl1

ALIGNMENTS

RESULT 1

US-08-748-485-1

Sequence 1, Application US/08748485

Patent No. 5817480

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice

APPLICANT: Guegler, Karl J.

APPLICANT: Goli, Suzya K.

APPLICANT: Murty, Lynn E.

TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:

ADDRESS: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/748,485

FILING DATE: Herewith

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0159 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 454 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: Consensus

CLONE: 1722180

US-08-748-485-1

Query Match

20.6%; Score 430.5; DB 2; Length 454;

Best Local Similarity 29.2%; Pred. No. 13e-30;
Matches 99; Conservative 68; Mismatches 137; Indels 35; Gaps 8;

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CY 31 GIRSTVIVIFLAASV--GNIVLALVLOKPKPOLLOVTFNFINLVLDTLLQISLVAPMV 88
DB 25 GVITIQFIAIVITIFVCLGNLIVITLVKKSVLTLNKNFVSLTSLNELLVVLVLPV 84
CY 89 VATSVPLFWPLNSHFCETALVSLTHLPFASVNTIVAVSVRYSLIHPLSYPSMCTOPPG 148
DB 85 VTSIIPFPMIFVWVWNCFSALVYLILSSASMLTGVIALDRYAVLVPMYKPKITGNPA 144
CY 149 YLLVGTWIVAILQSTPPLVYGWQAAFDERNALCSMIGWASPSYITLISVSVFIVPIIVM 208
DB 145 VMALVYIMLHSLICLFLPLFGWSSVFEDEFKMCVAMHFEFGYTAFWQICWALFPLVM 204
CY 209 IACVSVFCAAPRGCHALLVNVKPHSLVVKDGVENEDERGAKEKEPFQDEMMIFESLFP 268
DB 205 LVYVGFIFVAP-----VKAPVHCGTVIVVERDACTGVPKNS---STSTSSG 251
CY 269 SPPNS-----NSNPLPFCVYVYAKVFIILFSYVLSTGPY-CFLAVLAW--VDVET 319
DB 262 SPRNAPCGVAVSAN-----CCKALITLVLGAMVWVGFMVIVIASALWKSVSF 364
CY 320 QVPQVITITITLWFLQCCIHPRVYGVMEKTIKEIQDM 358
DB 305 SLETTA---TWLSPASAVCHPLVGLMKNKTVKELLGM 339

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RESULT 2

US-08-467-568-2
Sequence 2, Application US/08467568

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? PATENT NO. 5817477
? GENERAL INFORMATION:
? APPLICANT: SOPPET, DANIEL R
? TITLE OF INVENTION: ADRENBERGIC RECEPTOR
? NUMBER OF SEQUENCES: 13
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Carella, Byrne, Bain, Giffillan, Cecchi,
? STREET: 6 Becker Farm Road
? CITY: Roseland
? STATE: NJ
? COUNTRY: USA
? ZIP: 07068-1739
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/467,568
? FILING DATE: 06-JUN-1995
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
? NAME: Ferraro, Gregory D
? REGISTRATION NUMBER: 36,134
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-994-1700
? REFERENCE/DOCKET NUMBER: 325800-324
? INFRINGEMENT FOR SEQ ID NO: 2
? SEQUENCE CHARACTERISTICS:
? LENGTH: 529 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-467-568-2

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Query Match 19.5%; Score 409; DB 2; Length 529;
Best Local Similarity 28.5%; Pred. No. 1.3e-28;
Matches 103; Conservative 67; Mismatches 146; Indels 46; Gaps 10;

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DB 14 SNLREEGEGEAGASSPSSPSPLSSP-----FLSA--WGNLIVITLVYKKS 56
CY 61 QLOQVTFNFINLVLDTLLQISLVAPMVVATSVPLFWPLNSHFCETALVSLTHLPFASV 120
DB 57 YLLTSLNKNFVSLTSLNELLVVLVLPFVVTSSIRREMIFGVWVWNCFSALVYLILSSASMI 116
CY 121 TIVVAVDPRYSILHPLSYPSMCTOPPGYLLLYGTWIVAILQSTPPLVYGWQAAFDERPA 180
DB 117 TLGYIALDRYAVLVPMYKPKITGNRAVMALVYIMLHSLICLPLPLFGWSSVFEDEFKMW 176
CY 181 LGSMTWASPSYITLISVSVFIVPIIVMIACVSVFCAAPRGCHALLVNVKPHSLVVKD 240
DB 177 MCVAMHFEFGYTAFWQICWALFPLVMVLCYGPVIFRVAR-----VKAPVHCGTVV 228
CY 241 CVENEDERGAKEKEPFQDEMMIFESLPPSPNSNG--NPPLPCCYQAKAVFIILFSVY 299
DB 229 IVE-EDAQRTGRK-----NSTSTSSGPRRNAPCGVAVSANQCKALITLVLGAM 280
CY 309 LSLGPY-CFLAVLAW--VDVETQVPCWVITITLWFLQCCIHPRVYGVMEKTIKEIQ 356
DB 281 VTWGPVWVIVIASALWKSVSFLETTA---TWLSPASAVCHPLVGLMKNKTVKELL 336
CY 357 DM 358
DB 337 GM 338

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RESULT 3

US-09-030-582-2
Sequence 2, Application US/09030582

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? PATENT NO. 5994506
? GENERAL INFORMATION:
? APPLICANT: SOPPET, DANIEL R
? TITLE OF INVENTION: ADRENBERGIC RECEPTOR
? NUMBER OF SEQUENCES: 13
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Carella, Byrne, Bain, Giffillan, Cecchi,
? STREET: 6 Becker Farm Road
? CITY: Roseland
? STATE: NJ
? COUNTRY: USA
? ZIP: 07068-1739
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/030,582
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/467,568
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Ferraro, Gregory D
? REGISTRATION NUMBER: 36,134
? REFERENCE/DOCKET NUMBER: 325800-324
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 201-994-1700
? REFERENCE/DOCKET NUMBER: 325800-324
? INFRINGEMENT FOR SEQ ID NO: 2
? SEQUENCE CHARACTERISTICS:
? LENGTH: 529 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-030-582-2

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Query Match 19.5%; Score 409; DB 2; Length 529;
Best Local Similarity 28.5%; Pred. No. 1.3e-28;

CT-US94-09051-2

SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids

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;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 466 amino acids

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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-334-698-6

Query Match 17.7%; Score 371.5; DB 1; Length 466;
Best Local Similarity 26.9%; Pred. No. 2.5e-25;
Matches 109; Conservative 77; Mismatches 180; Indels 39; Gaps 11;

DB 5 SGNASDSNCTQP--PAPVNISKAILLGVILGGLLFGVLGNLVLILSVACHRHLSVTH 62
QY 68 RPIFNLLVTDLLQISLVAPWVAVTSVPLFWPLNSHPTALVSLTHFAFASVNTIVVAV 127
DB 63 YVIVNLAADLLTSTVLPFSAIFEVLYGMAFGRVCNIMADVLCCTASIMGLCIISI 122
QY 128 DRYLSIHPLSYSPKMTQRRGYLLVGTWIVALLQSTPPLVGMQGAFFERNALCSMIG 187
DB 123 DRYIGVSYPLRPPTIVTQPPGMALICVMALSLVISTGPLFGMPQGA-PEDETIQI--N 179
QY 188 ASPSTILSVSFIVIPILVIMACYSVFCAPRQ---HALLYNYPHGLEPVNCTVE 243
DB 180 EEPGYVLFSAIGSFYLLFALILVMYGRVYVAVAPRSPGLRSGLKTGSDGCVTLFHPK 239
QY 244 NEDEEG---AEKKEEPQDEMNIFESLPSPFNNSNPFLPRCYCCAKAVFIILFXY 298
DB 240 NAFAGGSGMASAKTKTHSVPL---LKFSPFR-----FAAKTLGIIVGCF 281
QY 299 VLSIGPYCFLLAVLWVAVDTQVPCWVITIIYLFLOCCHIPVYGYMKTIKKEIQDM 358
DB 282 VLCLWLPF-FLVMPIGSPFDPKPSSETVFKIVFWLGYLNSCINPIIYPCSSQCFYAFQV 340
QY 359 LK-KFPCKEKPKPK---DSHPDLPGTEGGTEGKI-VPSYSATF 397
DB 341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKMDVRIIVGSRETF 385

RESULT 6

US-08-228-932-6
Sequence 6, Application US/08228932

Patent No. 5578611

GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,

APPLICANT: Theresa A. Branche, John M. Metzger and Paul F. Hartig

TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN

TITLE OF INVENTION: PROSTATIC HYPERPLASIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/228,932

FILING DATE: 13-APR-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: (212) 422523 COOP UI

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-228-932-6

Query Match 17.7%; Score 371.5; DB 1; Length 466;
Best Local Similarity 26.9%; Pred. No. 2.5e-25;
Matches 109; Conservative 77; Mismatches 180; Indels 39; Gaps 11;

QY 8 STRESNSHTCMPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKPOLLOVTH 67
DB 5 SGNASDSNCTQP--PAPVNISKAILLGVILGGLLFGVLGNLVLILSVACHRHLSVTH 62
QY 68 RPIFNLLVTDLLQISLVAPWVAVTSVPLFWPLNSHPTALVSLTHFAFASVNTIVVAV 127
DB 63 YVIVNLAADLLTSTVLPFSAIFEVLYGMAFGRVCNIMADVLCCTASIMGLCIISI 122
QY 128 DRYLSIHPLSYSPKMTQRRGYLLVGTWIVALLQSTPPLVGMQGAFFERNALCSMIG 187
DB 123 DRYIGVSYPLRPPTIVTQPPGMALICVMALSLVISTGPLFGMPQGA-PEDETIQI--N 179
QY 188 ASPSTILSVSFIVIPILVIMACYSVFCAPRQ---HALLYNYPHGLEPVNCTVE 243
DB 180 EEPGYVLFSAIGSFYLLFALILVMYGRVYVAVAPRSPGLRSGLKTGSDGCVTLFHPK 239
QY 244 NEDEEG---AEKKEEPQDEMNIFESLPSPFNNSNPFLPRCYCCAKAVFIILFXY 298
DB 240 NAFAGGSGMASAKTKTHSVPL---LKFSEK-----FAAKTLGIIVGCF 281
QY 299 VLSIGPYCFLLAVLWVAVDTQVPCWVITIIYLFLOCCHIPVYGYMKTIKKEIQDM 358
DB 282 VLCLWLPF-FLVMPIGSPFDPKPSSETVFKIVFWLGYLNSCINPIIYPCSSQCFYAFQV 340
QY 359 LK-KFPCKEKPKPK---DSHPDLPGTEGGTEGKI-VPSYSATF 397
DB 341 LRIQCLCRKQSSKHALGYTLHPPSQAVEGQHKMDVRIIVGSRETF 385

RESULT 7

US-08-468-939-6
Sequence 6, Application US/08468939

Patent No. 5714381

GENERAL INFORMATION:

APPLICANT: Jonathan A. Bard et al.

TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic

TITLE OF INVENTION: Receptors and Uses Thereof

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,939

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41337-1B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526

INFORMATION FOR SEQ ID NO: 6:

1

1

Journal of Management Inquiry 25(4) 391-408

FILING DATE: 21-AUG-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 41337 A FCT US/JFW/ECB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0526
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 466 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-406-855A-6

Query Match: 17.7%, Score 371.5, DB 2, Length 466,
 Best Local Similarity: 26.9%, Freq. No. 2.5e-25;
 Matches: 109, Conservative: 77, Mismatches: 180, Indels: 39, Gaps: 11;

CY 8 STEPNSSHTWPLSPMPISLAHGIIPSTVLVIFLAASFVNIVLAVIQKQQLQVTH 67
 5 SGNADSSNGTGF PAFVNISKAILLVILGGLIPGVLDNIILVLSVACHPHLSVTH 62
 DB 68 RIFNLVTDLQISLVAPWVAVTSVLEFPLNSHFCALVSLTHFAFASNTIIVASV 127
 DB 63 YVIVLVAADLLTSTVLPFSALFEVLGVAAPGVACNTMAADVLCCTASINGCLTISI 122
 CY 128 DRYLSIHTPLSPKMGKQKGYLLVGTWIVAILQSTPLVYWGQAFERNALCSKMG 187
 DB 123 DRYIGVSYPLPYPTIVQPGMLALCVWALSLVLSIGPLGMRPA-DEDTICQI-N 179
 CY 188 ASPEYTLISVSEFVILVIMACYSVFCNAPRQ---HALLVNPHSLVPPVQDVE 243
 DB 180 EEPGVVLSALGSYLLFLAILLVYCYVVAAPRERGLKSLKLTSTSECVTLPIHR 239
 CY 244 NEDEEG...AEYFEFGQEMNIFESLPFSPNSNRTLPFCYCAKAVYFIIFSY 298
 DB 240 NAFAGSSMAKATHTHSVPL...LKFSPEK-----KAAKTLGIWVGEF 281
 CY 293 VLSGPGYCLAVLAWVAVETQVQWVITIIIMLFPGCCIHVYVGYKHTIYEQDM 358
 DB 282 VLWMLFF-FLVWFGSPFPEPEPELVEFVFWLYLNSCINFIIPQSSQEPYKQNV 340
 CY 359 LK-KFCEKEKPKE---DSHPDLGTGEGTEGKI-VPSYSATF 397
 DB 341 LRIQCLCKKSSKHALGYTLHPGQAVEGQHKMWRPIVGSRET 385

RESULT 10
 US-08-722-190-6
 Sequence 6, Application us/08722190
 Patent No. 5990128
 GENERAL INFORMATION:
 APPLICANT: Charles Gluchowski, Carlos C. Porray, George
 APPLICANT: Chiu, Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
 TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
 TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DUNHAM LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.24
 CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/08/722,190
 FILING DATE: 4-APR-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 41879-D-FCT US/JFW/AGL
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 466 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-722-190-6

Query Match: 17.7%, Score 371.5, DB 2, Length 466,
 Best Local Similarity: 26.9%, Freq. No. 2.5e-25;
 Matches: 109, Conservative: 77, Mismatches: 180, Indels: 39, Gaps: 11;

CY 8 STEPNSSHTWPLSPMPISLAHGIIPSTVLVIFLAASFVNIVLAVIQKQQLQVTH 67
 5 SGNADSSNGTGF PAFVNISKAILLVILGGLIPGVLDNIILVLSVACHPHLSVTH 62
 DB 68 RIFNLVTDLQISLVAPWVAVTSVLEFPLNSHFCALVSLTHFAFASNTIIVASV 127
 DB 63 YVIVLVAADLLTSTVLPFSALFEVLGVAAPGVACNTMAADVLCCTASINGCLTISI 122
 CY 128 DRYLSIHTPLSPKMGKQKGYLLVGTWIVAILQSTPLVYWGQAFERNALCSKMG 187
 DB 123 DRYIGVSYPLPYPTIVQPGMLALCVWALSLVLSIGPLGMRPA-DEDTICQI-N 179
 CY 188 ASPEYTLISVSEFVILVIMACYSVFCNAPRQ---HALLVNPHSLVPPVQDVE 243
 DB 180 EEPGVVLSALGSYLLFLAILLVYCYVVAAPRERGLKSLKLTSTSECVTLPIHR 239
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 DB 240 NAFAGSSMAKATHTHSVPL...LKFSPEK-----KAAKTLGIWVGEF 281
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 CY 359 LK-KFCEKEKPKE---DSHPDLGTGEGTEGKI-VPSYSATF 397
 DB 341 LRIQCLCKKSSKHALGYTLHPGQAVEGQHKMWRPIVGSRET 385

RESULT 11
 US-08-244-354-6
 Sequence 6, Application US/08244354
 Patent No. 601819
 GENERAL INFORMATION:
 APPLICANT: Charles Gluchowski, et al.
 APPLICANT: Chiu, Theresa A. Brancheck, John M. Wetzel and Paul R. Hartig
 TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
 TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DUNHAM LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.24

OPERATING SYSTEM: PC-DOS/MS-DOS

ZIP: 10036
COMPUTER READABLE FORM:

1 MEDIUM TYPE: Floppy disk
 2 COMPUTER: IBM PC
 3 OPERATING SYSTEM: PC-DOS/MS-DOS
 4 SOFTWARE: Patent in release #1124
 5 CURRENT APPLICATION DATA:
 6 APPLICATION NUMBER: US/09/444,783
 7 FILING DATE:
 8 CLASSIFICATION:
 9 ATTORNEY/AGENT INFORMATION:
 10 NAME: white, John P.
 11 REGISTRATION NUMBER: 28,678
 12 REPRESENTATIVE NUMBER: 41878 AA
 13 TELECOMMUNICATION INFORMATION:
 14 TELEPHONE: (212) 278-6450
 15 TELEFAX: (212) 391-6525
 16 TELEX:
 17 INFORMATION FOR SEQ ID NO.: 6:
 18 SEQUENCE CHARACTERISTICS:
 19 LENGTH: 466 amino acids
 20 TYPE: amino acid
 21 TOPOLOGY: linear
 22 MOLECULE TYPE: protein
 23
 24 US-09-444,783-6

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Best Local Similarity	26.98	Prod No.	2.58e-25			
Matches	109	Conservative	77	Mismatches	180	Gaps
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RESULT 14 1 1
US-09-688-415-6
; Sequence 6, Application US/09688415
; Patent No. 6448011
; GENERAL INFORMATION:
; APPLICANT: Bard, Jonathan A
; APPLICANT: Forray, Carlos
; APPLICANT: Weishank, Richard L
; TITLE OF INVENTION: DATA BROADCASTING HUMAN ALPHA 1 APPENDICULAR PROSTHESIS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 4133732a
; CURRENT APPLICATION NUMBER: US/09/688,415
; CURRENT FILING DATE: 2009-10-16
; PRIOR APPLICATION NUMBER: 09/474,551
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 21

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; SOFTWARE: Patencin Ver. 2.1
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; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-688-415-6

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Pb	190	E;E;P;G;V;L;F;S;A;I;G;S;T;P;A;I;L;I;V;M;C;V;V;V;V;A;V;P;E;S;O;L;K;S;I;G;L;T;Y;S;D;E;Q;U;L;P;I;H;P			219		
QY	244	N;E;D;E;G	..	A;E;K;E;E;F;O;E;M;N;I;F;E;S;L;P;F;S;F;N;S;H;P;L;P;C;Y;C;V;A;V;I;F;I;I;F;S;Y	298		
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Pb	282	V;L;C;M;L;F;F;L;M;P;I;O;S;E;F;F;P;K;S;E;T;E;F;K;I;V;F;W;G;Y;L;N;S;C;I;N;P;I;Y;P;O;S;Q;E;F;F;A;F;A;V					340
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 466 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04203-6

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Query Match      17.7%; Score 371.5; DB 5; Length 466;
Best Local Similarity 26.9%; Pred. No. 2.5e-25;
Matches 109; Conservative 77; Mismatches 180; Indels 39; Gaps 11;

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QY 68 RFIENLVTDLQISIVAPWVAVTSVPLFMPPLNSHCTALVSLTHLFAPASVNTIVVSV 127
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QY 128 DRYLSTIHPDLPSPKMTORRGVLLYGTVIIVAILOSTPPLYGWGOAFDERNALCSMIWG 187
   123 DRYIGVSYPLRPTIVTORRGIMALLCVWALSIVISIGPLFGWRQPA-PEDETICQI--N 179
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   180 FEPGVLPFSAIGSFYLPALILVMYCRVYVAKRESRGKSGLTKDSDSEQVTLRIHRK 239
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   240 NAPAGSGMASAKTYTHFSVRL---LKFSREK-----KAAKTIIGIVVGC 281
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   282 VLCWLPF-FLVMPIGSFPPDPKPSSETVFKIVFWLGYLNSCINPIIYPCSSQEFKKAFC 340
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Db

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 Job time : 33 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2003, 11:08:20 ; Search time 13 Seconds
(without alignments)
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Title: US-09-841-741-2

Perfect score: 2093
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Searched: 140259 seqs, 2554876 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	409	19.5	529	10	US-09-951-622-2
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6	366.5	17.5	466	10	US-09-951-622-11
7	326.5	15.6	501	10	US-09-951-622-9
8	326.5	15.6	522	9	US-10-185-991-2
9	324.5	15.5	472	9	US-10-166-101-3
10	321	15.3	451	10	US-09-993-844-6
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19	297	14.2	445	10	US-09-989-861-16

20	287	13.7	241	10	US-09-864-761-38226	Sequence 38226, A
21	277	13.2	460	10	US-09-989-861-18	Sequence 18, Appl
22	275	13.1	460	9	US-10-166-101-4	Sequence 4, Appl
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27	268.5	12.8	471	10	US-08-681-219-30	Sequence 30, Appl
28	268.5	12.8	471	10	US-09-929-313-2	Sequence 2, Appl
29	267.5	12.8	413	10	US-09-811-286-2	Sequence 2, Appl
30	267.5	12.8	413	10	US-09-951-622-12	Sequence 12, Appl
31	267.5	12.8	413	10	US-09-951-622-12	Sequence 12, Appl
32	267.5	12.8	413	10	US-09-951-622-12	Sequence 12, Appl
33	267.5	12.8	413	10	US-09-951-622-12	Sequence 12, Appl
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38	261	12.5	387	10	US-09-989-861-2	Sequence 2, Appl
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41	259	12.4	601	10	US-09-782-980-84	Sequence 84, Appl
42	259	12.4	222	10	US-09-884-430-8	Sequence 8, Appl
43	259	12.4	366	9	US-09-911-005-4	Sequence 4, Appl
44	258.5	12.4	382	10	US-09-992-331-9	Sequence 9, Appl
45	258	12.3	362	9	US-09-992-331-13	Sequence 5, Appl
					US-09-992-331-8	Sequence 13, Appl
					US-09-992-331-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-791-932-112
; Sequence 112, Application US/09791932
; Publication No. US2003003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiesch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US2003003451A1 G Protein-Coupled Receptors. Cross-Referenc
; FILE REFERENCE: 00325-US1
; CURRENT APPLICATION NUMBER: US/09791, 932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861

```

PRIORITY FILING DATE: 2000-06-23
PRIORITY APPLICATION NUMBER: 60/194,344
PRIORITY FILING DATE: 2000-04-03
PRIORITY APPLICATION NUMBER: 60/218,337
PRIORITY FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 112
LENGTH: 508
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-932-112

Query Match          96.7%; Score 2024; DB 9; Length 508;
Best Local Similarity 78.1%; Pred. No. 1,2e-176;
Matches 397; Conservative 1; Mismatches 0; Indels 110; Gaps 1;

QY 1 MTSTCTNSTRESNSSHQTMPLSKMPLSLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSSHQTMPLSKMPLSLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
QY 61 QLVQVTRNPFNLVTDLQISLVAPWVATSVPLFMPLNSHFCTALVSLTHLFAFASVN 120
DB 61 QLVQVTRNPFNLVTDLQISLVAPWVATSVPLFMPLNSHFCTALVSLTHLFAFASVN 120
QY 121 TIVVSVDRYLSIIHPLSPSKMTQRGVLVLLGTWIVAILQSTPPLVGMGOAFDERNA 180
DB 121 TIVVSVDRYLSIIHPLSPSKMTQRGVLVLLGTWIVAILQSTPPLVGMGOAFDERNA 180
QY 121 TIVVSVDRYLSIIHPLSPSKMTQRGVLVLLGTWIVAILQSTPPLVGMGOAFDERNA 180
DB 121 TIVVSVDRYLSIIHPLSPSKMTQRGVLVLLGTWIVAILQSTPPLVGMGOAFDERNA 180
QY 181 LCSMTWGSAPSTTILSVSFYIPLVIMTACYSVVFCAARQHALLVNKRHSLEVAKD 240
DB 181 LCSMTWGSAPSTTILSVSFYIPLVIMTACYSVVFCAARQHALLVNKRHSLEVAKD 240
QY 241 CVENDEEGAEKKEEFQDE..... 259
DB 241 CVENDEEGAEKKEEFQDE..... 259
QY 241 CVENDEEGAEKKEEFQDE..... 259
DB 241 CVENDEEGAEKKEEFQDE..... 259
QY 260 ..... 259
DB 260 ..... 259
QY 101 POSPEVESSTVASDQSMGKEGSTVKEENSMKADKRTVEVNOCSIDLGBDMEFGEDDI 360
DB 101 POSPEVESSTVASDQSMGKEGSTVKEENSMKADKRTVEVNOCSIDLGBDMEFGEDDI 360
QY 260 ..... 310
DB 260 ..... 310
QY 161 NPSRDVEAVNIPESLPSPRNSNPNPLPCYQCAAKYIFIIISYVSLGVCFLAV 420
DB 161 NPSRDVEAVNIPESLPSPRNSNPNPLPCYQCAAKYIFIIISYVSLGVCFLAV 420
QY 311 LAVWVDETVQVQWVITIIIMLFELQCCIHPRVYGYMKTIKKEIQDMLKKFCKEPRK 370
DB 421 LAVWVDETVQVQWVITIIIMLFELQCCIHPRVYGYMKTIKKEIQDMLKKFCKEPRK 370
QY 421 LAVWVDETVQVQWVITIIIMLFELQCCIHPRVYGYMKTIKKEIQDMLKKFCKEPRK 370
DB 421 LAVWVDETVQVQWVITIIIMLFELQCCIHPRVYGYMKTIKKEIQDMLKKFCKEPRK 370
QY 371 EDSHPDLPGTEGTEGKIYPSYDSATFP 398
DB 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508

RESULT 2
US-09-791-932-68
Sequence 68, Application US/09791932
Publication No. US20030003451A1
GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
APPLICANT: Parodi, Luis A.
APPLICANT: Hiebsch, Ronald P.
APPLICANT: Lind, Peter
APPLICANT: Kayles, Paul S.
APPLICANT: Ruff, Valerie
APPLICANT: Huff, Rita M.
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: No. US20030003451A1 G Protein-Coupled Receptors Cross-Referen
FILE REFERENCE: 00325 US1
CURRENT APPLICATION NUMBER: US/09791932
PRIORITY FILING DATE: 2001-02-23
PRIORITY APPLICATION NUMBER: 60/184,305
PRIORITY FILING DATE: 2000-02-23

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PRIORITY APPLICATION NUMBER: 60/184,304
PRIORITY FILING DATE: 2000-02-23
PRIORITY APPLICATION NUMBER: 60/184,303
PRIORITY FILING DATE: 2000-02-23
PRIORITY APPLICATION NUMBER: 60/184,397
PRIORITY FILING DATE: 2000-02-23
PRIORITY APPLICATION NUMBER: 60/184,247
PRIORITY FILING DATE: 2000-02-23
PRIORITY APPLICATION NUMBER: 60/188,880
PRIORITY FILING DATE: 2000-03-13
PRIORITY APPLICATION NUMBER: 60/217,369
PRIORITY FILING DATE: 2000-07-11
PRIORITY APPLICATION NUMBER: 60/217,370
PRIORITY FILING DATE: 2000-07-11
PRIORITY APPLICATION NUMBER: 60/218,492
PRIORITY FILING DATE: 2000-07-20
PRIORITY APPLICATION NUMBER: 60/186,810
PRIORITY FILING DATE: 2000-03-03
PRIORITY APPLICATION NUMBER: 60/188,064
PRIORITY FILING DATE: 2000-03-09
PRIORITY APPLICATION NUMBER: 60/186,457
PRIORITY FILING DATE: 2000-03-02
PRIORITY APPLICATION NUMBER: 60/213,861
PRIORITY FILING DATE: 2000-06-23
PRIORITY APPLICATION NUMBER: 60/194,344
PRIORITY FILING DATE: 2000-04-03
PRIORITY APPLICATION NUMBER: 60/218,337
PRIORITY FILING DATE: 2000-07-14
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 68
LENGTH: 204
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-932-68

Query Match          37.9%; Score 794; DB 9; Length 204;
Best Local Similarity 99.4%; Pred. No. 4.4e-65;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHQTMPLSKMPLSLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
DB 47 MTSTCTNSTRESNSSHQTMPLSKMPLSLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 106
QY 61 QLVQVTRNPFNLVTDLQISLVAPWVATSVPLFMPLNSHFCTALVSLTHLFAFASVN 120
DB 107 QLVQVTRNPFNLVTDLQISLVAPWVATSVPLFMPLNSHFCTALVSLTHLFAFASVN 166
QY 121 TIVVSVDRYLSIIHPLSPSKMTQRGVLVLLGTWIV 158
DB 167 TIVVSVDRYLSIIHPLSPSKMTQRGVLVLLGTWIV 204

RESULT 3
US-09-828-644-115
Sequence 115, Application US/09828644
Patent No. US20020015998A1
GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
TITLE OF INVENTION: No. US20020015998A1 G Protein-Coupled Receptors
FILE REFERENCE: 00196US1
CURRENT APPLICATION NUMBER: US/09828,644
PRIORITY FILING DATE: 2001-04-06
PRIORITY APPLICATION NUMBER: 60/195,150
PRIORITY FILING DATE: 2000-04-06
PRIORITY APPLICATION NUMBER: 60/195,099
PRIORITY FILING DATE: 2000-04-06
PRIORITY APPLICATION NUMBER: 60/195,151
PRIORITY FILING DATE: 2000-04-06
PRIORITY APPLICATION NUMBER: 60/195,148
PRIORITY FILING DATE: 2000-04-06
PRIORITY APPLICATION NUMBER: 60/195,093
PRIORITY FILING DATE: 2000-04-06

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PRIOR APPLICATION NUMBER: 60/195,098
 PRIOR FILING DATE: 2000-04-06
 PRIOR APPLICATION NUMBER: 60/230,149
 PRIOR FILING DATE: 2000-09-05
 NUMBER OF SEQ ID NOS: 117
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 115
 LENGTH: 242
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-828-644-115

Query Match 36.8%; Score 769.5; DB 10; Length 242;
 Best Local Similarity 81.5%; Pred. No. 9,4e-63;
 Matches 145; Conservative 7; Mismatches 19; Indels 7; Gaps 2;

QY 228 NVKRSLEVRVDC---VENEDEGAKEKEFODE---MNIPESLPSSRNSNSNPPLP 280
 Db 4 SMKAKGRTEVNOCSIDLGEDEDFEGEDDINFSEDDVEAVNIPESLPSSRNSNSNPPLP 63
 QY 281 RCYCKAAKVFIIIFSYVLSGPGCFGLAVAVWVDETQVPOWVITIIIMLFLOCCIH 340
 Db 64 RCYCKAAKVFIIIFSYVLSGPGCFGLAVAVWVDETQVPOWVITIIIMLFLOCCIH 123
 QY 341 PYYVGYMKTIKKELIOMDKKPFCKEKPKEKSHPDLPCTEGTEGKIVPSYDSTP 398
 Db 124 PYYVGYMKTIKKELIOMDKKPFCKEKPKEKSHPDLPCTEGTEGKIVPSYDSTP 181

RESULT 4
 US-09-951-622-2
 Sequence 2, Application US/09951622
 Patent No. US20020106734A1
 GENERAL INFORMATION:

APPLICANT: Daniel R. Soppet et al.
 TITLE OF INVENTION: ADRENERGIC RECEPTOR
 FILE REFERENCE: PF128D2C1
 CURRENT APPLICATION NUMBER: US/09/951,622
 CURRENT FILING DATE: 2001-09-14
 PRIOR APPLICATION NUMBER: 09/339,244
 PRIOR FILING DATE: 1999-06-24
 PRIOR APPLICATION NUMBER: 09/030,582
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 08/467,568
 PRIOR FILING DATE: 1995-06-06
 PRIOR APPLICATION NUMBER: PCT/US94/09051
 PRIOR FILING DATE: 1994-08-10
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 2
 LENGTH: 529
 TYPE: PRT
 ORGANISM: human
 US-09-951-622-2

Query Match 19.5%; Score 409; DB 10; Length 529;
 Best Local Similarity 28.5%; Pred. No. 1.8e-29;
 Matches 103; Conservative 67; Mismatches 146; Indels 46; Gaps 10;

QY 6 TNSTRE-----SNSSHTCMPLSKMPISLHGIIIRSTVLVIFLASFVGNITVLALVQRKP 60
 Db 14 SNLREGEGRGASSPSSSPSSPSSP-----FLSA--MGNLIVITLVYKS 56
 QY 61 OLOVNRFTFNLLVDLLOISLAPVAVATVPLEFPLNSHFCALVSLTHLPAFASVN 120
 Db 57 YLITSNKVFISLITLNFSLSVLDPVVVSSIRREWIFGVWCMFSLALYLLISSSML 116
 QY 121 TIVVSVDRYLSIHLPSYSKMTORRGVLLGTWVAILLOSTPPIYXGQAAFDPERNA 180
 Db 117 TUGVLAIDRYAVLVYVPMKLTGNRAVWALVYIMHSLGLCPPLFGSSVVEYGENKW 176
 QY 181 LCSMIMGASPSTIISVSVFTIVPLVIMACYSVVFCAAROHALLVNVHSLSEVAVKD 240

Db 177 MCVAAHREPGYTAFWQICALFPFLVMLVGYFIFRVAR-----VAKPVHCGTIV 228
 QY 241 CVENDEGAKEKEFODEMNIPESLPSSRNSNS--NPPLRCYCKAAKVFIIIFSYV 299
 Db 229 IVE-EDACRTGRK-----NSTSTSSGRRNARQGVVYSANQCKALLITLVLAQFM 280
 QY 300 ISLGPY-CFLAVLAW--VDVETQVPOWVITIIIMLFLOCCIHPPYVGYMKTIKKELI 356
 Db 281 VTWGPYVWVITASEALMGKSSVPSLETWA---TWLSFASAVCHPILYIGLMNIVREKEL 336
 QY 357 DM 358
 Db 337 GM 338

RESULT 5
 US-10-185-991-6
 Sequence 6, Application US/10185991
 Publication No. US20030022900A1
 GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, et al.
 TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN PROSTATIC HYPERPLASIA
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DUNHAM LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/185,991
 FILING DATE: 28-Jun-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/444,783
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 466 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-185-991-6

Query Match 17.7%; Score 371.5; DB 9; Length 466;
 Best Local Similarity 26.9%; Pred. No. 4.1e-26;
 Matches 109; Conservative 77; Mismatches 180; Indels 39; Gaps 11;

QY 8 STRESNSHTCMPLSKMPISLHGIIIRSTVLVIFLASFVGNITVLALVQRKPQLOVNR 67
 Db 5 SGNASDSSNCTOP--PAPVNISKAILLGVILGLLTFGLNIIIVLISVACHRHHSVTH 62
 QY 68 RPIFNLVITDLOISLAPVAVATVPLEFPLNSHFCALVSLTHLPAFASVNTIVVSV 127
 Db 63 YIIVNLAVADLLITSTVLPFAIFEVLGYWAFGRVFCNIMAAVDVLCCTASIMGCLTISI 122
 QY 128 DRYLSIHLPSYSKMTORRGVLLYGTWVAILLOSTPPIYXGQAAFDPERNALCSMIMG 187

Db 123 DRYIGVSVPLRPPTVTQGRGMLALCVMALSLVLSIGLFGMRQPA-PEDETICQ--N 179
 QY 188 ASPSTIISVSFFIYPLIVMIACYSVVFCAARQ---HALLYNKRHLEVRKDCVE 243
 Db 180 EEPGVLFSLSGFYLPLAILVMYCRVYVAVKESRGKSGKTKDSEQVTLRIHK 239
 QY 244 NEDDEG---AEKKEEFODEMNIPESLPSSRRNSNPFLLPCYCKAKAVIIFIISY 298
 Db 240 NAPAQSGSMASAKTHTHSVRL-----LKFSREK-----KAKKTLCIIVGCF 281
 QY 299 VLSIGPYCFILAVLAVWVDETQVPCQWVITIIWLFLQCCIHRYVGYMKTIKKEI 358
 Db 292 VLSIGPYCFILAVLAVWVDETQVPCQWVITIIWLFLQCCIHRYVGYMKTIKKEI 340
 QY 359 LK-KEFCEKEPKPE---DSHDLPTGEGTEGKI-VPSYDSATF 397
 Db 341 LPIGCLPPQSSKHALGYTLHPSCAVEGQHKMWNIPVGSRETF 385

RESULT 6

US-09-951-622 11
 ; Sequence 11, Application US/09951622
 ; Patent No. US20020106734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Daniel P. Soppet et al.
 ; TITLE OF INVENTION: ADPENERGIC PECEPTOR
 ; FILE REFERENCE: PFI28D2C1
 ; CURRENT APPLICATION NUMBER: US/09/951,622
 ; CURRENT FILING DATE: 2001-09-14
 ; PRIOR APPLICATION NUMBER: 09/339,244
 ; PRIOR FILING DATE: 1999-06-24
 ; PRIOR APPLICATION NUMBER: 09/030,582
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 08/467,568
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: PCT/US94/09051
 ; PRIOR FILING DATE: 1994-08-10
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 466
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-09-951-622-11

Query Match 17.5%, Score 366.5, DB 10, Length 466,
 Best Local Similarity 26.7%, Pred. No. 1,2e-25;
 Matches 109; Conservative 76; Mismatches 182; Indels 39; Gaps 10;

QY 8 STRENSSHTCMPISCMPLSLAHGIIIRSTVLVIFLAASFVGNIVLALVLCPRQLQV 67
 Db 5 SNARSSNSTQTP--PAPNISKAILLGVILGILLFGVGNILVILSVACHHLHSVTH 62
 QY 68 PFIPIVLVLDLQISLVAWVAVTSVPLFPLNSHCTALVSLTHLFAFASVNTIIVASV 127
 Db 63 YIIVLAVADLILTSVLPFSAIFELVGVAPGRVPCNTMAADVLCCTASIMGLCISI 122
 QY 128 DRYISIIHPLSYPSKMTQRRGYLLLYGTWIVALLQSTPPLVGMQQAFFDPNALCSMI 187
 Db 123 DRYIGVSVPLRPPTVTQGRGMLALCVMALSLVLSIGLFGMRQPA-PEDETICQ--N 179
 QY 188 ASPSTIISVSFFIYPLIVMIACYSVVFCAARQ---HALLYNKRHLEVRKDCVE 243
 Db 180 EEPGVLFSLSGFYLPLAILVMYCRVYVAVKESRGKSGKTKDSEQVTLRIHK 239
 QY 244 NEDDEG---AEKKEEFODEMNIPESLPSSRRNSNPFLLPCYCKAKAVIIFIISY 298
 Db 240 NAPAQSGSMASAKTHTHSVRL-----LKFSREK-----KAKKTLCIIVGCF 281
 QY 299 VLSIGPYCFILAVLAVWVDETQVPCQWVITIIWLFLQCCIHRYVGYMKTIKKEI 358
 Db 292 VLSIGPYCFILAVLAVWVDETQVPCQWVITIIWLFLQCCIHRYVGYMKTIKKEI 340

QY 359 LKKEFCEKEPKPEKDS---HDLPTGEGTEGKI-VPSYDSATF 397
 Db 341 LPIGCLPPQSSKHALGYTLHPSCAVEGQHKMWNIPVGSRETF 385

RESULT 7

US-09-951-622-9
 ; Sequence 9, Application US/09951622
 ; Patent No. US20020106734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Daniel R. Soppet et al.
 ; TITLE OF INVENTION: ADPENERGIC PECEPTOR
 ; FILE REFERENCE: PFI28D2C1
 ; CURRENT APPLICATION NUMBER: US/09/951,622
 ; CURRENT FILING DATE: 2001-09-14
 ; PRIOR APPLICATION NUMBER: 09/339,244
 ; PRIOR FILING DATE: 1999-06-24
 ; PRIOR APPLICATION NUMBER: 09/030,582
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 08/467,568
 ; PRIOR FILING DATE: 1995-06-06
 ; PRIOR APPLICATION NUMBER: PCT/US94/09051
 ; PRIOR FILING DATE: 1994-08-10
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-09-951-622-9

Query Match 15.6%, Score 326.5, DB 10, Length 501,
 Best Local Similarity 27.7%, Pred. No. 5.6e-22;
 Matches 96; Conservative 58; Mismatches 157; Indels 35; Gaps 10;

QY 29 AHGIIPTSTVLVIFLAASFVGNIVLALVLCPRQLQVNPFIPIVLVLDLQISLVA 88
 Db 52 AAGVGVGVFILAAFIIMAAAGNLVILSVACNRHLQTVNYFVLNVAVDLILSATVLP 111
 QY 89 VATSVPLFPLNSHCTALVSLTHLFAFASVNTIIVASVDRSLIHPISPSKMTQRRG 148
 Db 112 ATMEVLGFMARAFQCDVMAADVLCCTASILSTCTISVDPRVGYPHSLKYAINTPEPA 171
 QY 149 YLLIYGTWIVALLQSTPPLVGMQQAFFDPNALCSMIWASPSYTIISVSFFIYPLIV 207
 Db 172 AAILLWVAVLAVSVGFLQWMEFVPEDEP--FCGITEEA--GYAVFSSVCSFYLPXAV 227
 QY 208 MIACYSVVFCAAR--PQHALLYNKRHS-----LFVAVYPCVENEDEGAE... 254
 Db 228 IVWVYCRVYVAVTSVPLFPLNSHCTALVSLTHLFAFASVNTIIVASVDRSLIHPIS 285
 QY 255 EFCDEMNIPESLPSSRRNSNPFLLPCYCKAKAVIIFIISVYLSIGPYCFILAVLAW 314
 Db 286 TFRSLISV-RLKFSREK-----KAKKTLCIIVGCFVPLGS- 330
 QY 315 VDVETQVPCQWVITIIWLFLQCCIHRYVGYMKTIKKEI 360
 Db 331 LPIGCLPPQSSKHALGYTLHPSCAVEGQHKMWNIPVGSRETF 385

RESULT 8

US-10-185-991-2
 ; Sequence 2, Application US/10185991
 ; Publication No. US20030022900A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles Gluchowski, et al.
 ; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
 ; TREAT BENIGN PROSTATIC HYPERPLASIA
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: COOPER & DUNHAM LLP
 ; STREET: 1185 Avenue of the Americas


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? CURRENT FILING DATE: 2002-06-10
? PRIOR APPLICATION NUMBER: 09/246,075
? PRIOR FILING DATE: 1999-02-05
? PRIOR APPLICATION NUMBER: 08/483,222
? PRIOR FILING DATE: 1995-06-07
? PRIOR APPLICATION NUMBER: 08/117,006
? PRIOR FILING DATE: 1994-08-22
? PRIOR APPLICATION NUMBER: PCT/US93/00149
? PRIOR FILING DATE: 1993-01-08
? PRIOR APPLICATION NUMBER: 07/817,920
? PRIOR FILING DATE: 1992-01-08
? NUMBER OF SEQ ID NOS: 13
? SOFTWARE: PatentIn Ver. 2.0 - beta
? SEQ ID NO 3
? LENGTH: 422
? TYPE: prt
? ORGANISM: Homo sapiens
US-10-166-101-3

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? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 572 amino acids
?     TYPE: amino acid
?     TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 2:
? 5S-10-185-991-2

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	Best Local Similarity	25.78%	Score 326.5	DB 9	Length 572
	Matches 96	Conservative 58	Mismatches 157	Indels 35	Gaps 107
QY	29	AGGIIRSTVLVIFLAAEFVGNIVLALVQRRKPOLLOQNRFFENLNYMDLQISLVAPV	88		
DB	94	AGGVGVGVFLAAFLIMVAGLTVLISVACNRHQIQTNYNFIYVLAVADLLISATVLPSS	153		
QY	89	VATSVLPFLFWFLNHSCEALVSLTHLFAFASVNTIVVQSVDRYLSIHPESYPSKXTORRG	148		
DB	154	ATMEVLGFMAFGRAFCVQWMAVDVLCCTASTLSLCTISVDYVGVGRHSIKYPAIMTERKA	213		
QY	149	YLLIYGTWIVAILQSTPEPLYGWCQ-AAFDEENALCSMIWGAQSPSTIISVSEFVILIV	207		
DB	214	AALIALIMVVALVAVSVGPLGWMKEPVPDPER--FCGIITEEA--GYAVFSSVCSYFLPMAV	269		
QY	208	MLACYSVVFCAAR-RQALLINYKRRHS-----LEVRVQDCVENEDDEGAEE---KKE	254		
DB	270	IYVYKRVYVVAASTRSLGAVKREBGKASEVVLRIHCRGAATGAD--GAHGMRSAKH	327		
QY	255	EPQDENNIPESLPPSRNNSNSNPPLPRCYOQKAKVFIIFIIISYVLSLGPCTPLAVAVW	314		
DB	328	TRRSSLSLV-RLLEFSREK-----KAAKTLAVGVGVFLCMFPFFFLVLPGS-	372		
QY	315	VVETQVQPMVFIIFIIYVFLQCCIHPIYVYGVNKKTIKKGIQDMX	360		
DB	373	LPPQLKPSGVKPIVFWLQGFNACVNPDLIPCCSRREKRAFLRLIR	418		

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RESULT 10
US-09-993-844-6
; Sequence 6, Application US/099993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephanie A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 03072-026
; CURRENT APPLICATION NUMBER: US/09/993,844
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 451

```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: amino acid sequence of SH1A1-V2P chimera
OTHER INFORMATION: expressed from the pEAR1-1/SH1A1 vector
US-09-933-844.6

Query Match 15.3% Score 321, DB 10, Length 451;
Best Local Similarity 23.0%, Freq No. 1,6e+21;
Matches 190, Conservative 72, Mismatches 182, Indels 72, Gaps 8;

26 ISAAHIIPTSLVIFLAASFVN--IVLAVIQPPQLQVTPNPEIFNLVTLQISL 83
31 VIVSYQVITSLILGLICAVLGNACVVAIALER--SLQVANYLISLAVTDLWAVL 88
84 VAVVAVTSVLEFNLNHFCAVLSLHLFASFNTIVVSVDPYLSIHPLSPSK 143
89 VLVMAIVQVANKWTLQVTLDELFLALVQCTSSILCLALALPQWMTTFEIVNPE 148
144 TQPRGYLLYGMIVAILQSTPPYGMQGAFFERNALCSMIGASPSYTLISVSEIV 203
149 TPRPAALISITWLTGFIISTPRMIGWTP--FQSPNACTISKHGYTIYTPGAFY 206
204 FLVYIAITSVFVAFS FSAALLINVFHSLFV 237
207 FLIMLVYGRIFFAAPRPIPTVYVEVTZATPHASPAFPKSVNDESGFHWEL 246
229 VQDCEDEEGAEYEEFQDEMIPESYF.....P 270
267 VESTRGMALANBAVFGTGTGALVTVFHFVGNSTHFLSEAAFTFCAPASFPHR 326
272 ECHNRPFLFVYVKAAPVYFIIISVSLISFYFLAVLAVWVETQPCWVITII 336
327 PNAEVPFMAVAPERTVYTLGIWGTFLCMLPEFVALVFPCESSCHMPFLALIN 386
331 WLFELCCIHPRVGVYMHPTVKEIQDMKPRCKPRKPRSHPLPGEGTEKIVP 390
387 WLVGNSTINVIYAVFHPFQNAFPIIKCNFQ.....AAAPGTPPSLGP 433
DB 391 SYDSAT 396
DB 434 QDESGT 439

RESULT 11
US-10-052-589.2
Sequence 2, Application US/10052589
Patent No. US2002013832A1
GENERAL INFORMATION:
APPLICANT: Zuscik, Michael
TITLE OF INVENTION: M-301 systems for neurodegenerative and cardiovascular disorders
FILE REFERENCE: 26473/04200
CURRENT APPLICATION NUMBER: US/10/052,589
CURRENT FILING DATE: 2002-01-19
PRIOR APPLICATION NUMBER: US 09/568,255
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2
LENGTH: 477
TYPE: PRT
ORGANISM: Mesocricetus sp.
US-10-052-589.2

Query Match 15.2% Score 319, DB 10, Length 497;
Best Local Similarity 26.0%, Freq No. 2.7e+21;
Matches 92, Conservative 70, Mismatches 162, Indels 30, Gaps 7,
DB 32 CONSTITUTEDVTRAISVGL...VCAAFILFAVCHILVILSVACNHNLTPTNYFVNL 87

74 LVTDLQISLVAPVAVTSVLEFNLNHFCTALVSLHLFASFNTIVVSVDPYLSI 133
88 AINDLLSFVLPFSATLEVLGWVLCGRIFCDIWAADVLCCTASILSLCMTIDRYIGV 147
134 IHLSTRSKYKQKRGKTYLLVGTWVALIISTFHYWGQAAFFPNALCSMIGASPSY 193
148 RYSLQVFTLVPRKAILALLSWLSTVSIIGPLGKPEAPND-DECGVT--EEPRYA 204
207 ILVSVFTVIFLYWVWVAVCVVCPAPPCNALI.....YVVRHSLFVYVQVENE 245
205 LFESLSGFITFLAVLVWYCPVIVAFETTKLEAGVKNENGRLLTPHSHYF--HE 262
246 DEGAEKKEFQDEMIPESLPSPPNSNPLPFCYCCAAVIFIIISVSLQPY 305
263 DLSSTFAKGNPPSSIAVVLFPSPER-----YAAKTLGIVCMFLICWLPF 310
DB 306 CFLAVLAWVADVETQVFWVITIIIMFLQCCIHPRVGVYMHPTVKEIQDM 359
DB 311 -FLALPGLSFLTLKPPDAVFYVFWLGYENSCINPITIPCSSKEFKAPWRIL 363

RESULT 12
US-09-951-622-10
Sequence 10, Application US/09951622
Patent No. US20020106734A1
GENERAL INFORMATION:
APPLICANT: Daniel R. Soppet et al.
TITLE OF INVENTION: ADENOPGIC RECEPTOR
FILE REFERENCE: F0182021
CURRENT APPLICATION NUMBER: US/09/951,622
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/339,244
PRIOR FILING DATE: 1999-06-24
PRIOR APPLICATION NUMBER: 09/070,582
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 08/467,568
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: PCT/US94/09051
PRIOR FILING DATE: 1994-08-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 10
LENGTH: 517
TYPE: PRT
ORGANISM: human
US-09-951-622-10

Query Match 15.2% Score 319, DB 10, Length 517;
Best Local Similarity 26.4%, Freq No. 2.8e+21;
Matches 92, Conservative 160, Mismatches 160, Indels 30, Gaps 7;
DB 14 SHTCMPLSKMFIISAHGIIPSTVIVFLAASFGNIVLAVIQPPQLQVTPNPEIFNL 73
32 SSSNTLP...CLDITVAISGLVLAFLPAIVANILIVISVACNHNLTPTNYFVNL 87
74 LVTDLQISLVAPVAVTSVLEFNLNHFCTALVSLHLFASFNTIVVSVDPYLSI 133
98 AMADLLSFVLPFSALDEVGVWVLCRIFCDIWAADVLCCTASILSLCMTIDRYIGV 147
134 IHLSTRSKYKQKRGKTYLLVGTWVALIISTFHYWGQAAFFPNALCSMIGASPSY 193
148 RYSLQVFTLVPRKAILALLSWLSTVSIIGPLGKPEAPND-DECGVT--EEPRYA 204
194 ILVSVFTVIFLYWVWVAVCVVCPAPPCNALI.....YVVRHSLFVYVQVENE 245
205 LFESLSGFITFLAVLVWYCPVIVAFETTKLEAGVKNENGRLLTPHSHYF--HE 262
246 DEGAEKKEFQDEMIPESLPSPPNSNPLPFCYCCAAVIFIIISVSLQPY 305
263 DLSSTFAKGNPPSSIAVVLFPSPER-----YAAKTLGIVCMFLICWLPF 310
DB 306 CFLAVLAWVADVETQVFWVITIIIMFLQCCIHPRVGVYMHPTVKEIQDM 359

Db 311 -FIALPLGSLFSTLKPDAVEKVVFWLGFNSCLNPIIYPCSSKEFKR 357

RESULT 13

US-10-185-991-4

Sequence 4, Application US/10185991
Publication No. US20030022900A1

GENERAL INFORMATION:

APPLICANT: Charles Guichowski, et al.

TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN PROSTATIC HYPERPLASIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/185,991

FILING DATE: 28-Jun-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/444,783

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 520 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-185-991-4

Query Match 15.2%; Score 319; DB 9; Length 520;

Best Local Similarity 26.4%; Pred. No. 2.8e-21;

Matches 92; Conservative 66; Mismatches 160; Indels 30; Gaps 7;

7;

Db 311 -FIALPLGSLFSTLKPDAVEKVVFWLGFNSCLNPIIYPCSSKEFKR 357

RESULT 14

US-10-080-960-25

Sequence 25, Application US/10080960

Publication No. US20020197695A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Meyers, Rachel

TITLE OF INVENTION: 80090, 52874, 52880, 63497, AND 33425

FILE REFERENCE: 38155-20044.00

CURRENT FILING DATE: US/10/080,960

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/242,040

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: US 60/241,992

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: US 60/242,637

NUMBER OF SEQ. ID NOS: 37

SOFTWARE: FastSeq for Windows Version 4.0

SEQ. ID NO 25

LENGTH: 259

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Consensus amino acid sequence

US-10-080-960-25

Query Match 14.3%; Score 299; DB 9; Length 259;

Best Local Similarity 23.2%; Pred. No. 7.7e-20;

Matches 76; Conservative 56; Mismatches 97; Indels 98; Gaps 8;

8;

QY 48 GNIVLALVLRKPKQLQVTRFENLVTDLQSLVAPVWVATSY--PLFWPLNSHCT 105

Db 1 GNLVILVILRTKRLPTNIFILNLAVADLLPLTLPPALVYLVGSGEDMPGSA LCK 60

QY 106 ALVSLTLFAPASVNTIVVSVDRYLSIHPISYPSKMTQ--RGYLLYGTWIVAILQST 164

Db 61 LVYALDVVMYASILLTLAISIDRYLAIVHPILYRRRTSPRAKAVIILVWVIALTLSTL 120

QY 165 PP-LYGMGQAA-----FDERNALCSMTIGASPSYTIISVVSFIVTPLI 206

Db 121 PPLRFSWKTVEBNGTLLVNVTVCLIDPEESTASVSTW--LRSYVLLSTLVGFLPL 178

QY 207 VMIACYSVVFCARROHALLVYVYKRHSLEVRVYDVENEDGAEKKEFEQDEMNIPESL 266

Db 179 VILVGYTRILRTLR----- 192

QY 267 PPSRRNSNPNPLPRCYOQKAKAVFIITIFSYLSIGPY-----CELAVALAVWVDV 317

Db 193 -----KAAKTLVAVVAVFVLCWLPYFIVLLDTLCLISIMSTCE L 233

QY 318 ETQVQWVITIIIMLFLOCCIHPIVYV 344

Db 234 ERVLPT-ALVLTMLAVVNSCLNPIIY 259

RESULT 15

US-10-012-140-27

Sequence 27, Application US/10012140

Publication No. US20030009017A1

GENERAL INFORMATION:

APPLICANT: leiby, Kevin R.

APPLICANT: Kapeller-Libermann, Rosana

APPLICANT: Gluckmann, Maria A.

TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND

TITLE OF INVENTION: 14354 METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: 18152004900
 CURRENT APPLICATION NUMBER: US/10/012,140
 CURRENT FILING DATE: 2001-11-08
 PRIOR APPLICATION NUMBER: 60/246,768
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 60/246,772
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 60/249,185
 PRIOR FILING DATE: 2000-11-15
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 27
 LENGTH: 259
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Consensus amino acid sequence
 US-10-012-140-27

Query Match: 143%, Score 299, DB 3, Length 259;
 Percent Similarity 23.28, Pred. No. 7,76,20;
 Matches 76; Conservative 56; Mismatches 97; Indels 98; Gaps 8;

QY 48 GNIVLALVLCQKFFQLLQVTFNFIENLVLTDLQISLAPWVATSV-PLFMPLNHFCT 105
 1 GNILVILVILTRKRLPTNIFILNLAVADLLFLTTPMALYLVGSEDMFGSALCK 60
 QY 106 ALVSLTHLFAFASVNTIVVSVKRYLSIHPLSYSPKMTQ-PPGYLLLYGTWIVAILQST 164
 61 LVTAADVNMVVASILLTAISIDPYLAIVHPLPYPPPTSPPAKVILLVWLALLSL 120
 QY 145 EP-LYGMQQA-----FDERNALQSMWASPSYTIISVVSFIVIPLI 206
 121 PPLIFSWKTYEEENGTLNVNTVCLIPPESTASVSTW--LPSYVLLSTLVGFLLPL 178
 QY 207 VMACYSVVFCAAPPQHALLYVNPHEVRYVDVENEDEGAEKKEFPQDEMNIPESL 266
 179 VLVGYTRILRLR----- 192
 QY 267 VYKRNNSNRPFLPKYQCKAKAKVIFIIIFSYVLSLGP-----CTLAVLAVWDV 317
 193 -----KAAKTLVAVVVFVLCWLPYFIVILLDTLCLSTIMSSSTCEL 233
 QY 318 ETOVQWVITIIIMLFLOCCIHPPVY 344
 234 ERVILPT-ALLVTLWLAVVNSCLNPIIY 259

Search completed: February 11, 2003, 11:11:37
 Job time: 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 11, 2003, 11:06:10 ; Search time 21 Seconds
(Without alignments)
1821.976 Million cell updates/sec

Title: US-09-841-741-2

Perfect score: 2093

Sequence: 1 MTSTSTNSRESNSSHCTMP.....GTEGTEGKIVPSYDSATFP 398

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	371	17.7	466	2	157959
2	366.5	17.5	429	2	S65656
3	366.5	17.5	466	2	JN0765
4	366.5	17.5	499	2	S65657
5	356.5	17.0	466	2	A35375
6	354	16.9	477	2	S71323
7	331.5	15.8	477	2	JH0315
8	326.5	15.6	501	2	JH0447
9	326.5	15.6	572	2	J13369
10	324	15.5	515	2	J15125
11	321.5	15.4	422	2	J13829
12	320.5	15.3	421	2	I49375
13	319	15.2	515	2	A40491
14	319	15.2	517	2	A45121
15	314.5	15.0	560	2	A38731
16	305	14.6	509	2	A47174
17	299	14.3	448	2	A47519
18	297	14.2	445	2	A48881
19	296.5	14.2	440	2	A35566
20	296	14.1	448	2	S36402
21	285	13.6	443	1	DYHND2
22	284	13.6	318	2	S38511
23	280.5	13.4	484	2	S48657
24	277.5	13.3	459	2	A43951
25	277	13.2	458	2	JU0616
26	276	13.2	450	2	T16079
27	276	13.2	564	2	A38271
28	275	13.1	460	2	A32605
29	274.5	13.1	400	2	S32804

30	273.5	13.1	444	1	DYBOD2	dopamine receptor
31	273	13.0	479	2	S33776	muscarinic acetylch
32	272.5	13.0	475	2	I53040	beta-2-adrenergic
33	271.5	13.0	418	2	C29514	muscarinic acetylch
34	271	12.9	444	1	DYMSD2	dopamine receptor
35	271	12.9	444	1	S08146	dopamine receptor
36	271	12.9	466	2	S36794	beta-1-adrenergic
37	270	12.9	488	2	T15941	hypothetical prote
38	269	12.9	477	1	ORHUB1	beta-1-adrenergic
39	269	12.9	479	2	S10127	muscarinic acetylch
40	268.5	12.8	400	2	A53281	beta-3-adrenergic
41	268.5	12.8	471	2	A43956	serotonin receptor
42	267.5	12.8	413	1	QRHUB2	beta-2-adrenergic
43	266.5	12.7	446	1	DYHND1	dopamine receptor
44	266	12.7	363	2	I50475	dopamine D1 recept
45	265.5	12.7	420	2	I51666	Mel-1c receptor su

ALIGNMENTS

RESULT 1

157959 alpha-1C adrenergic receptor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Apr-2000

C/Accession: 157959; 152862; PC2179

P/Laz, T.M.; Porray, C.; Smith, K.E.; Bard, J.A.; Vayssie, P.J.; Branchek, T.A.; Weisshant

Mol. Pharmacol. 46, 414-422, 1994

A/Title: The rat homologue of the bovine alpha 1C-adrenergic receptor shows the pharmacol

A/Reference number: 157959; PMID:95021119; PMID:7935320

A/Accession: 157959

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-466 <RES>

A/Cross-references: EMBL:U07126; NID:9595275; PIDD:AAA62866.1; PID:9595276

R/Stewart, A.F.; Rokosh, D.G.; Bailey, B.A.; Karns, L.R.; Chang, K.C.; Long, C.S.; Kariya

Cite. Res. 75, 796-802, 1994

A/Title: Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. alpha 1C,

A/Reference number: 152862; PMID:95008062; PMID:7923624

A/Accession: 152862

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-38, 'L', 40-66, 'G', 68-466 <RE2>

A/Cross-references: EMBL:U13368; NID:9555851; PIDD:AAA52103.1; PID:9555852

R/Rokosh, D.G.; Bailey, B.A.; Stewart, A.F.R.; Karns, L.R.; Long, C.S.; Simpson, P.C.

Biochem. Biophys. Res. Commun. 200, 1177-1184, 1994

A/Title: Distribution of alpha 1C-adrenergic receptor mRNA in adult rat tissues by RNase

A/Reference number: PC2179; PMID:94241969; PMID:8185565

A/Accession: PC2179

A/Molecule type: mRNA

A/Residues: 102-279 <ROK>

A/Experimental source: cardiac myocyte

C/Comment: This factor comprises a multigene family. As do alpha-2 and beta-adrenergic re

C/Suprafamily: vertebrate rhodopsin

C/Keywords: neurotransmitter receptor; transmembrane protein

F/26-42/Domain: transmembrane #status predicted <TM1>

F/73-89/Domain: transmembrane #status predicted <TM2>

F/104-120/Domain: transmembrane #status predicted <TM3>

F/147-163/Domain: transmembrane #status predicted <TM4>

F/195-211/Domain: transmembrane #status predicted <TM5>

F/276-292/Domain: transmembrane #status predicted <TM6>

F/306-323/Domain: transmembrane #status predicted <TM7>

Query Match 17.7% Score 371; DB 2; Length 466;
Best Local Similarity 26.1%; Pred. No. 1.3e-23;
Matches 106; Conservative 78; Mismatches 180; Indels 42; Gaps 10;

QY 7 NSTRSNSHTCMPSKPISLAHGIRSTVLVIFLAASFVGNIVLALVQKRPQLQVT 66
DB 7 NASBSNCTH-----PPAPVNISKALILGVLIIIFVGLNIVLISVACRHLSVT 61
QY 67 NRIFNLLVTLDIQISLVAFVWVATSVPLFWPLNSHFTALVSLTHLFAFASVNTIVVS 126

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Db 62 HYVLAADVADLLSTVLPFSALFEILGVMAGRFNCINMAADVLCCTASIMGLCTIS 121
QY 127 VDRYVSIITHPLSYBKMTRQRPQVLLYGTWIVAILOSTPPLYMGCAAFERNAICSMTW 186
Db 122 IDRYIGVGYPLRYFTVTCRQFVALLCVWVLSLVISIGTFCGMFOQA-PEDETIQCI 178
QY 187 GASPYSTLSVSVFVPIVIMVACSVVFCARPO-----HALLVNVKRSLEVRVDCV 242
Db 179 NEERGVYVLSALSGYVPLAILVMYCRVYVAKRPSRGKSLKPKDSKSEQVTLP 238
QY 243 ENEDEEG-----AEKREFFQCEMNIPESLPFSRNSNSHPPLFCYQCAAXVIFIIIFS 297
Db 239 KNVPAEGGVSSAKXKTHFSVRL-----LKFSREK-----KAAKTLGIWVGC 280
QY 298 VVLSGPGYCEPLAVLWVWVDETQVPOWVITIIIMLFLOCCHPVYGYMHNKIKKEIOD 357
Db 281 FVLCWLPF-FLVMPDGSFFPDKRPSETVFKIVFWLQYLNLCINPIIYPCSSQDFKAFQV 339
QY 358 MLKFFCKEYKPKEDS HPDLPGTEGTEGKI VPSYDSATF 397
Db 340 VLRIGCLPPPGSSKHALGYTLHPQSALFGQHNRWRIPIVGSSETF 395

```

RESULT 2

S65656
alpha-1C-adrenergic receptor splice form 3 - human

N/Alternate names: alpha-1C-adrenoreceptor isoform 3

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1996 #sequence_revision 22 Nov-1996 #extn_change 20-Jun-2000

C/Accession: S65656; S65654

R/Tanaka, T.

Submitted to the EMBL Data Library, July 1994

A/Reference number: S65656

A/Accession: S65656

A/Molecule type: mRNA

A/Residues: 1-429 <TAN>

A/Cross-references: EMBL:D32201, NID:3927210; PIDN:BA06900.1, PID:9927211

P/Hirasawa, A.; Shibata, K.; Horie, Y.; Takai, Y.; Ohtsuka, K.; Muramatsu, N.;

FEBS Lett. 363, 256-260, 1995

A/Title: Cloning, functional expression and tissue distribution of human alpha(1C)-adren

A/Reference number: S65654; MUID:9555557; PMID:7737411

A/Accession: S65654

A/Molecule type: mRNA

A/Residues: 424-429 <HIR>

A/Cross-references: EMBL:D32201

C/Genetics:

A/Gene: GDB:ADRA1C; ADRA11

A/Cross-references: GDB:128088; OMIM:104221

A/Map position: 8p21.8p11.2

C/Superfamily: vertebrate rhodopsin

C/Keywords: alternative splicing; neurotransmitter receptor

Query Match 17.5%; Score 366.5; DB 2; Length 429;

Best Local Similarity 26.7%; Pred. No. 2,8e+23;

Matches 108; Conservative 76; Mismatches 182; Indels 39; Gaps 10;

QY 8 STBSSNSHTCMPLSKMPSISLAHGIIRSTVLVFLAASVGNIVLVLQKRPQLQVTN 67

Db 5 SGNASDSSNCTQP--PAPVNIKSKALLGVILGLIFGVILGNILVLSVACHRHLSVTH 62

QY 68 REINFLVTDLQISLVAMPVWVATSVPLFWPLNSHCTALVSIITHLPAPASVTIVVSV 127

Db 63 YVIVMVAADLLTSTVLPFSALFEVLYGVMAGRFNCINMAADVLCCTASIMGLCTIS 122

QY 128 DRYVSIITHPLSYBKMTRQRPQVLLYGTWIVAILOSTPPLYMGCAAFERNAICSMTW 187

Db 123 DRYVSVSPLRPFTVTCRQFVALLCVWVLSLVISIGTFCGMFOQA-PEDETIQCI--N 179

QY 188 ASPSTILSVSVFVPIVIMVACSVVFCARPO-----HALLVNVKRSLEVRVDCV 243

Db 180 EEPGVVLSALSGYVPLAILVMYCRVYVAKRPSRGKSLKPKDSKSEQVTLP 238

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QY 244 NEDEEG-----AEKREFFQCEMNIPESLPFSRNSNSHPPLFCYQCAAXVIFIIIFS 298
Db 240 NARAGSGMSAKTKTHFSVRL-----LKFSREK-----KAAKTLGIWVGC 281
QY 299 VLSGPGYCEPLAVLWVWVDETQVPOWVITIIIMLFLOCCHPVYGYMHNKIKKEIOD 358
Db 282 VLCWLPF-FLVMPDGSFFPDKRPSETVFKIVFWLQYLNLCINPIIYPCSSQDFKAFQV 340
QY 359 LKFFCKEYKPKEDS-----HPDLPGTEGTEGKI-VPSYDSATF 397
Db 341 LRIQCLRRKSSKHALGYTLHPQSALFGQHNRWRIPIVGSSETF 395

```

RESULT 3

JN0765
alpha-1C-adrenergic receptor - human

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #extn_change 21-Jul-2000

C/Accession: JN0765; I84635; J02333; G01419

R/Hirasawa, A.; Horie, K.; Tanaka, T.; Takagaki, K.; Murai, M.; Yano, J.; Tsujimoto, G.

Biochem. Biophys. Res Commun. 195, 902-909, 1993

A/Title: Cloning, functional expression and tissue distribution of human cDNA for the al

A/Reference number: JN0765; MUID:93384619; PMID:8396931

A/Accession: JN0765

A/Molecule type: mRNA

A/Residues: 1-466 <HIR>

A/Cross-references: GB:U31774; NID:9666892; PIDN:AA859486.1; PID:9666893

R/Diehl, N.L.; Shreeve, S.M.

Eur. J. Pharmacol. 268, 393-398, 1994

A/Title: Identification of the alpha 1C adrenoreceptor in rabbit arteries and the human sa

A/Reference number: I47013; MUID:95104335; PMID:7805763

A/Accession: I84635

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 202-344 <DIR>

A/Cross-references: GB:S76001; NID:9313817; PIDN:AA14205.1, PID:94261905

R/Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Kutra, S.; Perkins-Barrow, A.; Borkowski, D.; S

Biochem. Biophys. Res Commun. 201, 1296-1304, 1994

A/Title: Cloning, expression and characterization of human alpha adrenergic receptors al

A/Reference number: J02333; MUID:94206402; PMID:8024574

A/Accession: J02333

A/Molecule type: mRNA

A/Residues: 1130, 'P', 132, 140, 'P', 142, 166, 'C', 168, 247, 'H', 249, 337, 'C', 339, 430, 'Q', 432, 466

A/Cross-references: GB:S70782; NID:3547223; PIDN:AA91163.1, PID:947220

R/Elleston, K.O.

Submitted to the EMBL Data Library, April 1994

A/Reference number: G06938

A/Accession: G01419

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 236-346, 'C', 348-430, 'Q', 432-466 <ELL>

A/Cross-references: EMBL:U08994; NID:9497243; PIDN:AA18783.1, PID:9497244

C/Comment: This protein plays critical roles in the regulation of a variety of physiolog

C/Genetics:

A/Gene: GDB:ADRA1C; ADRA11

A/Cross-references: GDB:128088; OMIM:104221

A/Map position: 8p21-8p11.2

A/Intons: 295/3

A/Note: the list of introns may be incomplete

C/Superfamily: vertebrate rhodopsin

C/Keywords: alternative splicing; glycoprotein; receptor; transmembrane protein

F/66-90/Domain: transmembrane #status predicted <TM1>

F/66-90/Domain: transmembrane #status predicted <TM2>

F/101-122/Domain: transmembrane #status predicted <TM3>

F/144-165/Domain: transmembrane #status predicted <TM4>

F/183-205/Domain: transmembrane #status predicted <TM5>

F/274-298/Domain: transmembrane #status predicted <TM6>

F/306-329/Domain: transmembrane #status predicted <TM7>

F/713/22/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.5%; Score 366.5; DB 2; Length 466;

Best Local Similarity 26.7%; Pred. No. 3,1e+23;

Matches 108; Conservative 76; Mismatches 182; Indels 39; Gaps 10;

QY 8 STESSNSHTCMPLSKMPLSLANGHIIIRSTVLVIFLAASFVGNIVLALVLRKPOLLOVTVN 67
 Db 5 SCNASDSSNCTOP--PAPVNIKAILLGVLGLILFGVLGNILVLISVACHRHLSVTH 62
 QY 68 RFIENLLVTDLLOISLVAWVAVATSVPLFWPLNSHFCCTALVSLTHLFAFASVNTIIVVSV 127
 Db 63 YIIVNLAVADLLITLSTVLPFSAIFEVLYGWAFCGRVPCNMAADVLCCTASIMGLCTIIS 122
 QY 128 DRYLSIIHPLSYPSKMTORRGVLLGYTWIALLQSTPPLYGWGOAFAFERNALCSMIWG 187
 Db 123 DRYIGSYPLRYPTIYTORRGMLALLCWMALSLVISTIGPLFGWRQPA-PEDETICQI--N 179
 QY 188 APPSYTILSVSEFIVPLIWMACYSVVFCAARQ----HALLYNVKNHSLERVDCVE 243
 Db 180 EEPGYVLFSAISFYPLAIIIMYCRVYVVAARESGRLSGKLTDKSDSEQVTLTHRK 239
 QY 244 NEDERG-----AEKKEFODEMNIPELSLPPSRNSNSNPPLPRCYOCKAKAVIFIIIFSY 298
 Db 240 NAPAAGSGMASAKTKTHFSVRL-----LKFSREK-----KAAKTGLIIVGCF 281
 QY 299 VLSLGPYCLAVLAVWVDVETQVPQWVITIIIMLFLOCCIHPIYVGYMHNKTIKKEIQDM 358
 Db 282 VLCWLPF-FLVMPIGSFPDPFKEFVFKIVFWLGLNSCINPIIYPCSSQEFKKAFOV 340
 QY 359 LKKFCEKPEPKEDS-----HPDLPTGEGTEGKI-VPSYDSATF 397
 Db 341 LRIOCLRRKQSSKHALGYTLHPHPSQAVEGQHKDWMVIRIPVGSRETF 385

RESULT 4

alpha-1C-adrenergic receptor splice form 2 - human
 N:Alternate names: alpha-1C-adrenoceptor Isoform 2
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 20-Jun-2000
 C:Accession: S65657, S65655

Submitted to the EMBL Data Library, July 1994
 A:Reference number: S65656
 A:Accession: S65657

A:Residues: 1-499 <TAN>
 A:Molecule type: mRNA
 A:Cross-references: EMBL:D32202; NID:G927208; PIDN:BAA06901.1; PID:G927209
 R:Hisatsawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.,
 FEBS Lett. 363, 256-260, 1995
 A:Title: Cloning, functional expression and tissue distribution of human alpha(1C)-adren
 A:Reference number: S65654; MUID:95255557; PMID:7737411
 A:Accession: S65655

A:Molecule type: mRNA
 A:Residues: 424-499 <HTR>
 A:Cross-references: EMBL:D32202
 C:Genetics: A:Gene: GDB:ADRA1C; ADRA1L1

A:Cross-references: GDB:128098; OMIM:104221
 A:Map position: 8p21-8p11.2
 C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 17.5%; Score 366.5; DB 2; Length 499;
 Best Local Similarity 26.7%; Pred. No. 3.3e-23;
 Matches 108; Conservative 76; Mismatches 182; Indels 39; Gaps 10;

8 STRENSSHTCMPLSKMPLSLANGHIIIRSTVLVIFLAASFVGNIVLALVLRKPOLLOVTVN 67
 Db 5 SCNASDSSNCTOP--PAPVNIKAILLGVLGLILFGVLGNILVLISVACHRHLSVTH 62
 QY 68 RFIENLLVTDLLOISLVAWVAVATSVPLFWPLNSHFCCTALVSLTHLFAFASVNTIIVVSV 127
 Db 63 YIIVNLAVADLLITLSTVLPFSAIFEVLYGWAFCGRVPCNMAADVLCCTASIMGLCTIIS 122
 QY 128 DRYLSIIHPLSYPSKMTORRGVLLGYTWIALLQSTPPLYGWGOAFAFERNALCSMIWG 187

Db 123 DRYIGSYPLRYPTIYTORRGMLALLCWMALSLVISTIGPLFGWRQPA-PEDETICQI--N 179
 QY 188 APPSYTILSVSEFIVPLIWMACYSVVFCAARQ----HALLYNVKNHSLERVDCVE 243
 Db 180 EEPGYVLFSAISFYPLAIIIMYCRVYVVAARESGRLSGKLTDKSDSEQVTLTHRK 239
 QY 244 NEDERG-----AEKKEFODEMNIPELSLPPSRNSNSNPPLPRCYOCKAKAVIFIIIFSY 298
 Db 240 NAPAAGSGMASAKTKTHFSVRL-----LKFSREK-----KAAKTGLIIVGCF 281
 QY 299 VLSLGPYCLAVLAVWVDVETQVPQWVITIIIMLFLOCCIHPIYVGYMHNKTIKKEIQDM 358
 Db 282 VLCWLPF-FLVMPIGSFPDPFKEFVFKIVFWLGLNSCINPIIYPCSSQEFKKAFOV 340
 QY 359 LKKFCEKPEPKEDS-----HPDLPTGEGTEGKI-VPSYDSATF 397
 Db 341 LRIOCLRRKQSSKHALGYTLHPHPSQAVEGQHKDWMVIRIPVGSRETF 385

RESULT 5

alpha-1-adrenergic receptor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
 C:Accession: A35375
 R:Schwinn, D.A.; Lomasney, J.W.; Lorenz, W.; Szklut, P.J.; Freneau Jr., R.T.; Yang-Feng,
 J. Biol. Chem. 265, 8183-8189, 1990
 A:Title: Molecular cloning and expression of the cDNA for a novel alpha-1-adrenergic rec
 A:Reference number: A35375; MUID:90243698; PMID:1970822
 A:Accession: A35375
 A:Molecule type: mRNA
 A:Residues: 1-466 <SCCH>
 A:Cross-references: GB:J05426; NID:G162663; PIDN:AAA30374.1; PID:G162664
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote

Query Match 17.0%; Score 356.5; DB 2; Length 466;
 Best Local Similarity 25.5%; Pred. No. 2.1e-22;
 Matches 108; Conservative 74; Mismatches 176; Indels 65; Gaps 10;

QY 7 NSTRENSSHTCMPLSKMPLSLANGHIIIRSTVLVIFLAASFVGNIVLALVLRKPOLLOVTVN 66
 Db 7 NASDSSNCTH-----PPPVNIKAILLGVLGLILFGVLGNILVLISVACHRHLSVTH 61
 QY 67 RFIENLLVTDLLOISLVAWVAVATSVPLFWPLNSHFCCTALVSLTHLFAFASVNTIIVVSV 126
 Db 62 HYIIVNLAVADLLITLSTVLPFSAIFELGYWAFGRVPCNMAADVLCCTASIMGLCTIIS 121
 QY 127 VDRYLSIIHPLSYPSKMTORRGVLLGYTWIALLQSTPPLYGWGOAFAFERNALCSMIW 186
 Db 122 DRYIGSYPLRYPTIYTORRGMLALLCWMALSLVISTIGPLFGWRQPA-PEDETICQI-- 178
 QY 187 GASPSYTLISVSEFIVPLIWMACYSVVFCAARQ----HALLYNVKNHSLERVDCV 242
 Db 179 NEERGVLVLFSAISFYPLIIMYCRVYVVAARESGRLSGKLTDKSDSEQVTLTHIR 238
 QY 243 ENDEBERG-----AEKKEFODEMNIPELSLPPSRNSNSNPPLPRCYOCKAKAVIFIIIFSY 297
 Db 239 KNAQVGGSGVTSKAKNTHFSVRL-----LKFSREK-----KAAKTGLIIVGCF 280
 QY 298 VLSLGPYCLAVLAVWVDVETQVPQWVITIIIMLFLOCCIHPIYVGYMHNKTIKKEIQD 357
 Db 281 FVLCWLPF-FLVMPIGSFPDPFKEFVFKIVFWLGLNSCINPIIYPCSSQEFKKAFOV 340
 QY 358 MLKKFCEKPEPKEDS-----EDSHPTL-----PTGEGTEGKI 388
 Db 340 VLRIOCLRRKQSSKHTLGYTLHAPSHVLEGGHDKDVRIPVGAETFYKISKIDGVEKMTI 399
 QY 389 VPS 391
 Db 400 FSS 402

RESULT 6

alpha-1A adrenergic receptor - Japanese medaka
S71323

C:Species: Oryzias latipes (Japanese medaka)
C:Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999
C:Accession: S71323

P:Yasutaka, A.; Abe, K.; Arai, S.; Emori, Y.
Eur. J. Biochem. 235, 501-507, 1996

A:Title: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Medaka
A:Reference number: S71323, MUID:96184522, PMID:8654394
A:Accession: S71323

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-477 <YAS>
A:Cross-references: EMBL:D63859
A:Note: it is uncertain whether Met-1 or Met-8 is the initiator
C:Superfamily: vertebrate rhodopsin

Query Match 16.9%; Score 354; DB 2; Length 477;
Best Local Similarity 28.0%; Pred. No. 3,66-22;
Matches 109; Conservative 63; Mismatches 193; Indels 24; Gaps 10;

12 SNSSHCTCMPLSKYKMSLAHGIIIPSTVIVIFLAASVGNVTLALVIOPKPQILQVTPPIF 71
18 SNGSHVLAP-----FLNIVKAVLVKVLGIFILEVIGNLTLLSVGHPHLCTVIVFIV 73

72 NLIVTDLLOLQILVAFWVAVTSVFLFWPLNSHPTCALVSLTHFAPASVNTIVVSVPEYL 131
74 NLAVADLLSLSTVLPFSAIFELDPWVFGVPCNIMAAVDVLCCTASISLGVISVDRI 133

132 SIHHPLSYSPKMKQPRVYLLVGTMTIVALLQSTPPLVGGQAAFDPRNALCSYIMWASPS 134
134 GVSYPPLRYPRIMKPRPALIAMLVLVLIISTGPLFWKKPR-PRDETGVCKTT--EEPG 190

192 YTLISVSPFVPIPLIVMACVSVVFCAPFQHALYNNVFNLSLVFVKDVEHEDEGAE 251
194 YALFSAVGSFYLPLALILAWYCPVYVAQTE-----SPGLKEGQKIEVSDSGVI 240

252 YPEEPQDEMIIPESLPSPSPNSNRPPLPCYQCYCAAKVIFITISVYSLGPGYCLAVL 311
241 LEMH PGNITVSEDEALPSRTHFALTLKFSREKFAAKTLGIIVGCFVLQWLP-FFLVL 297

312 AAWVDVETQVP-QWVITIIILPFIQCCIHPRVYVGMHTIKKEIDMLKFFCKEKP 370
298 PLGISPRAPRPSCTVFKETFWLGYFNSCINPIIYLCNSQEFKAPQSL-GVNCLKMTPR 356

371 EDSHPDLPGTEGGTEG-KIVPSYDSATPP 398
357 AHHN-HLSVGQSOTGGSLTSLDSKCAP 384

RESULT 7

TH0315

serotonin receptor 1A - rat
N:Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12 Feb. 1993 #sequence_revision 12 Feb. 1993 #text_change 13-Aug-1993
C:Accession: JH0315, A35181

R:Fujimura, Y.; Nelson, D.L.; Kashiwara, K.; Varga, E.; Ponske, W.P.; Yamamura, H.I.
Life Sci. 47, 127-132, 1990

A:Title: The cloning and sequence analysis of the rat serotonin-1A receptor gene.
A:Reference number: JH0315, MUID:90355775, PMID:2167416
A:Accession: JH0315

A:Molecule type: DNA
A:Residues: 1-422 <FUJ>

R:Albert, P.R.; Zhou, Q.Y.; Van Tol, H.H.M.; Bunzow, J.R.; Civelli, O.
J. Biol. Chem. 265, 5825-5832, 1990

A:Title: Cloning, functional expression, and mRNA tissue distribution of the rat 5-hydroxytryptamine receptor 1A.
A:Reference number: A35181, MUID:90202832, PMID:2156831
A:Accession: A35181

A:Molecule type: DNA
A:Residues: 1-372, S', 374-422 <Alb>
A:Cross-references: GB:J05276, NID:3202540; PIDR:AAA40612.1; PTD:3202541

C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
 F:37-62/Domain: transmembrane #status predicted <TM1>
 F:74-98/Domain: transmembrane #status predicted <TM2>
 F:109-134/Domain: transmembrane #status predicted <TM3>
 F:153-178/Domain: transmembrane #status predicted <TM4>
 F:255-277/Domain: transmembrane #status predicted <TM5>
 F:346-371/Domain: transmembrane #status predicted <TM6>
 F:379-404/Domain: transmembrane #status predicted <TM7>

Query Match 15.8%, Score 331.5; DB 2; Length 422;
 Best Local Similarity 24.4%; Pred. No. 2,5e+20;
 Matches 98; Conservative 69; Mismatches 163; Indels 71; Gaps 8;

QY 26 ISLAGIRSTLVLFVFLASFVGN--IVLALVQRKPOLQVTRFTFNLLVTLQLSL 83
 Db 31 VTFSSQVITSLGLTILFCFVGLNACVVAIALER--SLQNVNYYLGLSLAVTDLMASVL 88
 QY 84 VAPWVATSVLPFLPPLNSHFCALVSLTHLFAFASVNTIVVSVDRYLSIHPISYSEEM 143
 Db 89 VLPMAALVQLNKKTKLGQVTCDLFIALDVLCCTSSILHLCAIALDRYWAIDPIDYVNRK 148
 QY 144 TQPPGVLLYGVWVIAILQSTPLVGVGQGAAPERNALGSMWASQSYTLASVSVFI 203
 Db 149 TPPPMALISLTMVLGFLSIPMLGMPTP--EDSPDPACTTISKDHGYTLYSTFGAFYI 206
 QY 204 PLIVVYACYSVVFCAAFPGHATLYNVYFHSLEVPVD..... 249
 Db 207 PLLMLTVLYGR:FPAAP.....FPFKTPVKEVYFAGTSLGTSSAPPKKSLNGQGS 260
 QY 241QVERE.....DECAEKKKEFPQDEKMIPELFP PEPNHSNRP. 278
 Db 261 GDWPCAEENPAVTPPTNGAVPQGDDEATLEVLVHPVNSKEHLPLPSGSGSNVAPAC 320
 QY 279LPFGQCYAAVYIFLIFSVYVSLGVCCEFLAVAWDVEVQVEQW 324
 Db 331 LERKEPNAEAPRYMALAEPRKTVKTLGIIMGTFLICWLPFFVAVLVPRFENSCMDAT 390
 QY 335 VITTIIMFLFQCCHPYYVGYGMHTITKYEIQDMLKPKPK 365
 Db 381 LGATINMLGYSNLSLNFVIYAVFNKDFQNAFKKTIKCKPCR 421

RESULT 8
 JH0447
 alpha-1A-adrenergic receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
 C:Accession: JH0447
 R:Burns, J.F.; Whittaker, J.; Song, J.; Berelowitz, M.
 Biochem. Biophys. Res. Commun. 179, 1485-1490, 1991
 A>Title: Molecular cloning and sequencing of a cDNA encoding a human alpha 1A adrenergic
 A:Reference number: JH0447; MCID:3202892; PMID:1656955
 A:Accession: JH0447
 A:Molecule type: mRNA
 A:Residues: 1-501

 A:Cross-references: GR M76446; NID:3177806; PTDN:AAA35496.1; PTD:3177807
 A:Experimental source: hippocampus
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:56-79/Domain: transmembrane #status predicted <TM1>
 F:93-116/Domain: transmembrane #status predicted <TM2>
 F:128-151/Domain: transmembrane #status predicted <TM3>
 F:172-196/Domain: transmembrane #status predicted <TM4>
 F:210-233/Domain: transmembrane #status predicted <TM5>
 F:308-331/Domain: transmembrane #status predicted <TM6>
 F:339-363/Domain: transmembrane #status predicted <TM7>

Query Match 15.6%, Score 326.5; DB 2; Length 501;
 Best Local Similarity 27.7%; Pred. No. 8e+20;
 Matches 96; Conservative 58; Mismatches 157; Indels 35; Gaps 10;

29 AHGTRSTVLVFLAASFVGNIVALVQPPQQLQVTRFTFNLLVTLQLQSLAVAEW 88

Db 52 AAGVGVFLAALFMAVAGNLLVTLVACNRHQLTVINVTIVLAVADLLSATVLEPS 111
 QY VAVSVLEFNLNHFCAIYVSLTHLFAFASVNTIVVSVDRYSLIHPPLSPKMTORG 148
 Db 112 ATMEVTLGFMAFGAFCDVMAAVDLCTTASILSLCTISVDRYVGVHSLKYPALINTERKA 171
 QY 149 YLLVGTWVIALIQTTPPLYGWCQ-AAFDERNALCSMIMGASPSYTLISVSVFIVPLIV 207
 Db 172 AAILLMLVVALVSVGLPLGWKEPVPPDER--FCGITEEA--GYAVFSSVCSFYLLPMAY 227
 QY 208 MIACSVVFCAR-RQHALLVNVKHS-----LEVRYKDCVENDEEGAE-----KKE 254
 Db 228 IVMYICRYVVAARSTTRSLKAGVRRGKASEVLRHCRGAATGAD--GAHGRSAKCH 285
 QY 255 EFODEMNIPESLPPSRNSNSNPPLPRCYOCCAAYFIIFISVYSLGPLYCFLAVLAW 314
 Db 286 TFRSLSV-RLKFSREK-----KAAKTALVGVFVLCWPFPEFVPLGS- 330
 QY 315 VDVEQVPOWVITTIIMWFFLQCCIHPPYVGYMHKTIKEIDMLK 360
 Db 331 LFPQKPSGVFKVIFWLGYNFNSCVNPLIYPCSSREFKRAFLRLR 376

RESULT 9

139369

alpha-1A-adrenergic receptor - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 13-Aug-1999
 C/Accession: J139369; J02331

R/Ebershad, T.A.; Hirasawa, A.; Teujimoro, G.; Tanaka, T.; Yano, J.; Mineman, K.P.; M
 Mol. Pharmacol. 47, 977-985, 1995

A/Title: Cloning of the human alpha 1A-adrenergic receptor and inducible expression of
 A/Reference number: J139369; MUID:95265059; PMID:7746284

A/Accession: J139369

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-572 <RES>

A/Cross-references: GB:029952; NID:9914933; PIDN:BA00622.1; PID:9914934

R/Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
 Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994

A/Title: Cloning, expression and characterization of human alpha adrenergic receptors al

A/Reference number: J02331; MUID:94296402; PMID:8024574

A/Accession: J02331

A/Molecule type: mRNA

A/Residues: 1-30,'G','32-521','P','523-572 <WEI>

A/Note: the authors translated the codon CCC for residue 522 as Arg

C/Genetics:

A/Genes: GDB:ADRA1A; ADRA1; ADRA1R

A/Cross-references: GDB:118749; OMIM:104219

A/Map position: 20pter-20qter

A/Introns: 37/3

C/Superfamily: vertebrate rhodopsin

C/Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein

F/89-123/Domain: transmembrane #status predicted <TM1>

F/132-162/Domain: transmembrane #status predicted <TM2>

F/172-197/Domain: transmembrane #status predicted <TM3>

F/208-235/Domain: transmembrane #status predicted <TM4>

F/254-278/Domain: transmembrane #status predicted <TM5>

F/344-374/Domain: transmembrane #status predicted <TM6>

F/380-414/Domain: transmembrane #status predicted <TM7>

F/65,82/Binding site: carbohydrate (asn) (covalent) #status predicted

Db 154 ATMEVTLGFMAFGAFCDVMAAVDLCTTASILSLCTISVDRYVGVHSLKYPALINTERKA 213
 QY 149 YLLVGTWVIALIQTTPPLYGWCQ-AAFDERNALCSMIMGASPSYTLISVSVFIVPLIV 207
 Db 214 AAILLMLVVALVSVGLPLGWKEPVPPDER--FCGITEEA--GYAVFSSVCSFYLLPMAY 269
 QY 208 MIACSVVFCAR-RQHALLVNVKHS-----LEVRYKDCVENDEEGAE-----KKE 254
 Db 270 IVMYICRYVVAARSTTRSLKAGVRRGKASEVLRHCRGAATGAD--GAHGRSAKCH 327
 QY 255 EFODEMNIPESLPPSRNSNSNPPLPRCYOCCAAYFIIFISVYSLGPLYCFLAVLAW 314
 Db 328 TFRSLSV-RLKFSREK-----KAAKTALVGVFVLCWPFPEFVPLGS- 372
 QY 315 VDVEQVPOWVITTIIMWFFLQCCIHPPYVGYMHKTIKEIDMLK 360
 Db 373 LFPQKPSGVFKVIFWLGYNFNSCVNPLIYPCSSREFKRAFLRLR 418

RESULT 10

J01525

alpha-1B-adrenergic receptor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
 C/Accession: J01525; S08400

R/Gao, B.; Kunos, G

Gene 131, 243-247, 1993

A/Title: Isolation and characterization of the gene encoding the rat alpha 1B adrenergic

A/Reference number: J01525; MUID:94010315; PMID:8406017

A/Accession: J01525

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-515 <GNO>

A/Cross-references: GB:108610; NID:9202624; PIDN:AAA40647.1; PID:9202626

R/Voigt, M.M.; Kispert, J.; Chin, H.

Nucleic Acids Res. 18, 1053, 1990

A/Title: Sequence of a rat brain cDNA encoding an alpha-1B adrenergic receptor.

A/Reference number: S08400; MUID:9012094; PMID:2156222

A/Accession: S08400

A/Molecule type: mRNA

A/Residues: 1-202,'C','204-206','C','208-305','C','307-414','QK','417-439','C','441-483','ATA','487-

A/Cross-references: EMBL:X51585; NID:955557; PIDN:CAA53934.1; PID:955558

C/Genetics:

A/Introns: 317/1

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 15.5%; Score 324; DB 2; Length 515;
 Matches 93; Conservative 70; Mismatches 161; Indels 30; Gaps 7;

QY 14 SHTTCLSKMPLSLAHGIRSTVLVFLAASFGNIVLALVQKRGQLQVNRFTFNL 73
 Db 32 SNNSTLPQDVTIRALISVGL---VLGAFILFAIVGNILVTLVACNRHLETPNYFIVNL 87
 QY 74 LVTDLIQIOLVAPVAVATVPLFWPLNSHPCALVSLTHLFAFASVNTIVVSVDRYSLI 133
 Db 88 AIALDLSTFTVVPFSAITLLELGVWVGRIFCDIWAADVLCCTASILSLCAISIDRYIGV 147
 QY 134 IHPPLSPKMTORGRLGLLYGTWVIALIQTTPPLYGWCQAAPDERNALCSMIMGASSYT 193
 Db 148 RYSLQYPTLVTRKKAIALLSVWVLSVLSIGPLDQWKEPAPND--DKEGCVT--EEFVYA 204
 QY 154 ILSVSVFIVPLIWMACSVVFCARROHALL-----YVVKHSLLEVRYKDCVENE 245
 Db 205 LFSSLSGFYIPLAVILVMYICRYVVAARSTTRSLKAGVRRGKASEVLRHCRGAATGAD--GAHGRSAKCH 327
 QY 246 DEBGAKEEPEFODEMNIPESLPPSRNSNSNPPLPRCYOCCAAYFIIFISVYSLGPLY 305
 Db 263 DTLSSTAKGNNRPSIAVLFKFSREK-----KAAKTALVGVFVLCWPFPEFVPLGS- 372
 QY 306 CFLAVLAVVDVEQVPOWVITTIIMWFFLQCCIHPPYVGYMHKTIKEIDMLK 360

Accession	Protein Name	Organism	Length	Score	DB	Length	Score	DB
89	VLPMAALGVNKKMTLGGVATCDLFLALMDVLCCTSSILHLALADPRWALIDPLDYVKKP	148						
QY	144 TORGGYLLYGWIVAILOSTPPLYGMGGAPEDEBNALCMIMKASSTYLLSVSFVI	203						
149	TPPPAAALSLTMLIGLFLISIPMLGMPRP--EDSPDPACTISKDHQYTYSTFGAFYI	206						
204	FLIVIAIACSVVECAAR--SGHALHYHVFHSIFVE.....	237						
207	FLLLKLVLYGPRFPRAAFPRFPTVVRVYVETGADTFHACANAPCTGYCVVSGESGFNMLG	266						
QY	238VDCVENEEDEGAERKEEFQDEKNIPESLP-PS-----	270						
271	VESEPAIALVATYAVFVDCFLALEVIEVSPVNSQEPERFLFSEMTITTFVASEEPRE	326						
QY	271 PMSNNPRLPRVCYCCAAAVIFILIFSVYSLSPYCELAVALAVVAVETGYQAWITTI	330						
207	PAEAKPPVVALAPERTVTVTLGIMGTFLICWLPFPIVALVLPFCESCHMFTLIGALIN	386						
QY	331 WLFPIQCCIHPPVYGYMERTIKKEIQMDLKKPFCKE	366						
207	WLGSGNELNFIYAVFPRDFCAFPRTTYICPCPQ	422						
RESULT 12								
149375	serotonin receptor 1A - mouse							
A:Alternate names:	5-hydroxytryptamine receptor 1A (5-HT1A)							
C:Species:	Mus musculus (house mouse)							
C>Date:	02-Jul-1996 #sequence revision 02 Jul-1996 #text change 13 Aug-1999							
C:Accession:	149375; A57508							
F:Charest, A, Wainer, B H, Albert, P, P								
F:Neurosci. 13, 5164-5171, 1993								
A:Title:	Cloning and differentiation-induced expression of a murine serotonin1A receptor							
A:Reference number:	149375, PMID:94076013, PMID:8254366							
A:Accession:	149375							
A:Status:	preliminary, translated from GB/EMBL/DBD							
A:Molecule type:	mRNA							
A:Residues:	1-421 <CHA>							
A:Cross-references:	EMBL:U03201, NID:31066225, FIDR:MAA81519.1, PID:31066225							
F:Milikil, T M, Chen, Y, Gilbert, D, G, Moore, K J, Yu, L, Simon, M I, Copeland, N G								
F:Genomics 18, 175-184, 1993								
A:Title:	Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptor 1A							
A:Reference number:	A48909, PMID:94116980, PMID:82689218							
A:Accession:	A57508							
A:Status:	preliminary							
A:Molecule type:	mRNA							
A:Residues:	136-176, 177, 178-241, 242, 243-246, 247, 248-253, 254-303, 304-320, 321-322							
A:Cross-references:	GB:U03339							
C:Keywords:	G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein							
F:37-62/Domain:	transmembrane #status predicted <TM1>							
F:74-98/Domain:	transmembrane #status predicted <TM2>							
F:110-132/Domain:	transmembrane #status predicted <TM3>							
F:153-178/Domain:	transmembrane #status predicted <TM4>							
F:192-217/Domain:	transmembrane #status predicted <TM5>							
F:346-367/Domain:	transmembrane #status predicted <TM6>							
F:379-403/Domain:	transmembrane #status predicted <TM7>							
F:1011,124,30/Binding site:	carbohydrate (asn) (covalent) #status predicted							
F:109-187/Disulfide bonds:	#status predicted							
Query Match	15.3%	Score	320.5	DB	2	Length	421	
Best Local Similarity	24.3%	Pred. No.	2	Le-19				
Matches	98	Conservative	74	Mismatches	155	Indels	77	Gaps
QY	26 ISLHGITPSTVIVIFIAAPVFN--IVLALVLPQQLDQVTPRIFNLIVTDLLQSL	83						
DB	31 VFFSVQVITSLILGLTIFCAVAGNACVVAIALER--SLQNVAVYVILGSLAVTDLIMVSL	88						
QY	84 VAPWVAIVSPLPFWPLNSFCTALVSLTILFAFASVNTIVVGVDEYLSIINPLSYRKM	143						
DB	89 VLEPMALVGV							

QY 144 TORRGVLLLYGTWIVAILOSTPLPYGMOAFADEBNA-LGSMINGASPSYTLISVSFTIV 202
 Db 149 TPRRAALISLTWLTIGLILIPMLGW-RAPEBDSNPEECTI--SKDHGYITSTFGAFY 205
 QY 203 IPLIWIACSVVFCARROHALLVYVNRHSLVYV-- 239
 Db 206 IPLMLVLYGRIFRAAR-----FRIRKTVKVEKKAGAGTSFGTSAPPPKSLNPG 259
 QY 240 --DCVNEDE-----EGAEKKEEPODEMNIPE-----SLP-PSRRNSNPPL 279
 Db 260 SDDCRSAENRBAVGTFCANAVAGGEDATLEVIETVRHVGNSKQDPLPSSSGATSY--V 317
 QY 280 PRCY-----OCCAQVIFIIIFSVLSGYPCLAVLAWVDVETOV 321
 Db 318 PACLERKNERTEAKRKRMALAREKTVTKTIGIMGTFLCMLPFVIALVLPFCSSCHM 377
 QY 322 PQWVTIIIFLFOCCIPHYVGYMHTIKKEIQDMLKFFCK 365
 Db 378 PELLGATINWLGYSNLNLPVIAVYFNKDFONAFKIKCKPCR 421

RESULT 13

A40491
 Alpha-1-adrenergic receptor - golden hamster
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
 C:Accession: A40491
 R:Cotecchia, S.; Schwinn, D.A.; Randall, R.R.; Lefkowitz, R.J.; Caron, M.G.; Kobilka, B.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7159-7163, 1988
 A:Title: Molecular cloning and expression of the cDNA for the hamster alpha-1-adrenergic
 A:Reference number: A40491; MUID:89017157; PMID:2845398
 A:Accession: A40491
 A:Molecule type: mRNA
 A:Residues: 1-515 <COT>
 A:Cross-references: GB:040084; NID:9619407; PID:AAA58964.1; PID:9619408
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 15.2%; Score 319; DB 2; Length 515;
 Best Local Similarity 26.0%; Pred. No. 3.6e-19;
 Matches 92; Conservative 70; Mismatches 162; Indels 30; Gaps 7;

QY 14 SHTCMPLSKMPISLAHGIIRSTVIVIFLAASFVGNIVLALQKRPQLOQVTRFIFNL 73
 Db 32 SSNSTLP---QDITRAISVGLNFILFAIVGNILVILSVACNRHLRPTNYFIVNL 87
 QY 74 LVTDLQISLVAWVAVTSVPLFWPLNSHFTALVSLTHLPAFASVNTIVVSDRYLSI 133
 Db 88 AINDLLSFTVLPFSATLEVLGVWLGRIPCDIWAADVLCCTASILSLCAISIDRYIGV 147
 QY 134 IHPLSYPSKMTORRGVLLLYGTWIVAILOSTPLPYGMOAFADEBNA-LGSMINGASPSYT 193
 Db 148 RYSLQYPTLVTRKAILLALLSVWLVSTVISIGPLGWKEPAPND-DKECGVT--EEPFYA 204
 QY 194 ILSVSEFIVPLIWMVACSVVFCARROHALL-----YVVKRHSLEVRVDCVENE 245
 Db 205 LSSLSGSFYIPLAVILWYCRVYIVAKRTKNLEAGVWKEMSKETLTRHSGNF--HE 262
 QY 246 DEGAKEKEEPODEMNIPESLPSRRNSNPPLPRCYOCCAQVIFIIIFSVLSGYP 305
 Db 263 DTLSTKAKGHNPRSSIAVKLFKFSREK-----KAAKTLGIIVGMFLLCWLPF 310
 QY 306 CFLAVLAWVDVETOVPOWVTIIIFLFOCCIPHYVGYMHTIKKEIQDML 359
 Db 311 -FIALPLGSLFSTLKPDAVFKVFWLGYFNSCLNPIIPCSSKEKFAWRIL 363

RESULT 14

A45121
 Alpha-1B adrenergic receptor - human
 C:Species: Homo sapiens (man)
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Apr-2000
 A:Accession: A45121; J02332

R:Ramirez, C.S.; Denker, J.M.; Perez, D.M.; Galvin, R.J.; Riek, R.P.; Graham, R.M.
 J. Biol. Chem. 267, 21936-21945, 1992
 A:Title: Genomic organization and expression of the human alpha 1B-adrenergic receptor.
 A:Reference number: A45121; MUID:93016158; PMID:1328250
 A:Accession: A45121
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-517 <RAM>
 A:Cross-references: GB:M95990; NID:9178211
 A:Note: Sequence extracted from NCBI backbone (NCBI:116785)
 R:Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borokowski, D.; S.
 Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
 A:Title: Cloning, expression and characterization of human alpha adrenergic receptors
 A:Reference number: J02331; MUID:94296402; PMID:8024574
 A:Accession: J02332
 A:Molecule type: mRNA
 A:Residues: 1-158, 'P', 160-244, 'H', 246-314, 'F', 316-380, 382-517 <WEI>
 C:Genetics:
 A:Gene: GDB:ADR1A1B
 A:Cross-references: GDB:127901; OMIM:104220
 A:Map position: 5q31.1-5q33.2
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:39-72/Domain: transmembrane #status predicted <TM1>
 F:81-111/Domain: transmembrane #status predicted <TM2>
 F:121-146/Domain: transmembrane #status predicted <TM3>
 F:157-184/Domain: transmembrane #status predicted <TM4>
 F:203-227/Domain: transmembrane #status predicted <TM5>
 F:290-320/Domain: transmembrane #status predicted <TM6>
 F:326-360/Domain: transmembrane #status predicted <TM7>

Query Match 15.2%; Score 319; DB 2; Length 517;
 Best Local Similarity 26.4%; Pred. No. 3.6e-19;
 Matches 92; Conservative 66; Mismatches 160; Indels 30; Gaps 7;

QY 14 SHTCMPLSKMPISLAHGIIRSTVIVIFLAASFVGNIVLALQKRPQLOQVTRFIFNL 73
 Db 32 SSNSTLP---QDITRAISVGLNFILFAIVGNILVILSVACNRHLRPTNYFIVNL 87
 QY 74 LVTDLQISLVAWVAVTSVPLFWPLNSHFTALVSLTHLPAFASVNTIVVSDRYLSI 133
 Db 88 AINDLLSFTVLPFSATLEVLGVWLGRIPCDIWAADVLCCTASILSLCAISIDRYIGV 147
 QY 134 IHPLSYPSKMTORRGVLLLYGTWIVAILOSTPLPYGMOAFADEBNA-LGSMINGASPSYT 193
 Db 148 RYSLQYPTLVTRKAILLALLSVWLVSTVISIGPLGWKEPAPND-DKECGVT--EEPFYA 204
 QY 194 ILSVSEFIVPLIWMVACSVVFCARROHALL-----YVVKRHSLEVRVDCVENE 245
 Db 205 LSSLSGSFYIPLAVILWYCRVYIVAKRTKNLEAGVWKEMSKETLTRHSGNF--HE 262
 QY 246 DEGAKEKEEPODEMNIPESLPSRRNSNPPLPRCYOCCAQVIFIIIFSVLSGYP 305
 Db 263 DTLSTKAKGHNPRSSIAVKLFKFSREK-----KAAKTLGIIVGMFLLCWLPF 310
 QY 306 CFLAVLAWVDVETOVPOWVTIIIFLFOCCIPHYVGYMHTIKKEIQDML 359
 Db 311 -FIALPLGSLFSTLKPDAVFKVFWLGYFNSCLNPIIPCSSKEKFAWRIL 363

RESULT 15

A38731
 Alpha-1A adrenergic receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Apr-2000
 C:Accession: A38731; A53280
 R:Lomans, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Feng, T.L.;
 J. Biol. Chem. 266, 6365-6369, 1991
 A:Title: Molecular cloning and expression of the cDNA for the alpha-1A-adrenergic recept
 A:Reference number: A38731; MUID:91177889; PMID:1706716
 A:Accession: A38731
 A:Molecule type: mRNA

A:Residues: 1-560 <LOM>
 A:Cross references: GP MG6674, JID:302761, ECTN AAA63477.1, EID:302762
 A:Perez, D.M.; Plascik, M.T.; Graham, P.M.
 A:Pharmacol. 40, 876-883, 1991
 A>Title: Solution-phase library screening for the identification of rare clones: isolati
 A:Reference number A53280, M0102054, PMID:1661838
 A:Accession: A53280
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1 36, 'F', 38 58, 'I', 60 202, 'I', 204 305, 'R', 307 366, 'I', 368 370, 'I', 372-559 <F
 A:Experimental source: hippocampus
 A:Note: sequence extracted from NCBI backbone (NCBI:73541)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein coupled receptor; glycoprotein; transmembrane protein

Query March 15.08; Score 314.5; DB 2; Length 560;
 Best Local Similarity 27.58; Pred No 9,4e-19;
 Matches 94; Conservative 59; Mismatches 162; Indels 27; Gaps 8;

QY	29	ANGIIRSTVLVIFLASPVGNIVLALVLRKPOLQVTRNFIFNLVTDLLQISLVAPWV	88
DB	88	AGGVGVGVFLAFILTAVAGNLVLISVACNPHLQVTVYFIVLAVADLLSAVLPS	147
QY	89	VATSVPLPLPLNSHCTALVSLTHLFAPASVNTIVVSVDRILSIHPLSYESKMTQREG	148
DB	148	ATMEYLGFMAFGCTGCPDWAADVLCCTASTLSLCTISVDPVGVPHSLKYPAMTEPKA	207
QY	149	YLLAYGTWIVAILQSTPLRYWQ--AAFDENALCSMIGASPSYILSVSFIVPLIV	207
DB	208	AAITAILMAVALVAVSVGLLWKREPRPDER--FGGIT--EEVGYAIFSSVCSFYLPMAV	263
QY	208	MTAYGVVFCNAFEGHALYVYFPHSLSEVYVCGVENEDEGAE YKEEYQDENHIES	265
DB	264	IVMYCPYVAVPS-----TTPSLFAGIV---PPGKASEVVIPIHCPGAATSAG	311
QY	266	LFPCR FEGENRFLPCYGVGAAYVIFILISVYLSLSPYCLAVLAWVDVE	318
DB	312	YPGTSSRGHTLPSLSVPLLPSPREYFAATTAIVVGVFVLCWPPPFVYPLIGS-LFPQ	370
QY	419	TQVPQWVITITILFELQCTIHPYVYGVWHTIKKEIQMLK	360
DB	371	LKPSGVFFVIFWLVGFNCGVNPITYPGSSPEKPAFLPLP	412

Search completed: February 11, 2003, 11:10:40
 Job time : 23 secs